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1019.028 Million cell updates/sec

US-10-014-363-3 Perfect score:

1 APPRIEGRAPPRLICDSRVL.......NFLRGKLKLYTGEACRTGDR 174 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseq1980s:\* geneseq1990s:\* geneseq2000s:\* geneseq2001s:\* geneseq2003as:\* geneseq2003as:\* A\_Geneseq\_23Sep04:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES æ

	u c	Amino aci	Amino aci			Oligopept	Amino aci	Amino aci			Kb signal	Non-qlyco	Seguence	Recombina	Human erv	Human EPO	•~	Protein #	Human ery							
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#### ALIGNMENTS

Amino acid sequence of a modified human erythropoietin (EPO). ABB77898 standard; protein; 174 AA. (first entry) 07-0CT-2002 ABB77898; ABB77898 

Human, erythropoietin, BPO, glycoprotein, reticulocyte production, red blood cell production, anaemia, chronic renal failure, acquired immunodeficiency syndrome; AIDS, cancer, bone marrow, committed erythroid progenitor.

Synthetic. Homo sapiens.

 .8 /note= "proteolytic cleavage site"
 .174 /note= "EPO protein" Location/Qualifiers WO200249673-A2 Cleavage-site Protein

08-DEC-2001; 2001WO-EP014434. 27-JUN-2002.

20-DEC-2000; 2000EP-00127891.

Schurig HE, Hilger B, (HOFF ) HOFFMANN LA ROCHE & CO AG F. Engel A, Franze R, Burg J, Wozny M;

3

Tischer

WPI; 2002-566640/60.

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

Disclosure; Page 38-39; 40pp; English.

The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

WPI; 2002-566640/60.

Wozny M;

N-PSDB; ABL59289

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specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein is no vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma reabidence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients immunodeficiency syndrome (AIDS) and for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
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100.0%; Score 894; DB 5; Length 174;
Best Local Similarity 100.0%; Pred. No. 3.1e-91;
Matches 174; Conservative 0; Mismatches 0; Indels C
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    .27
    /note= "secretion signal peptide"

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The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The state of secrification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycoprotein is covalently linked to a poly(cetylend elycol) group. The glycoprotein is covalently linked to a poly(cetylend elycol) group. The EPO glycoprotein production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma regidence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when comparated to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients cundergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
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/note= "proteolytic cleavage site"
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Matches 174; Conservative
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The present sequence tepperature number at protecting teach, protein. The EPO was extended at the N-terminal by a proteclytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired in munderficients (TRF) and prophylaxis of diseases correlated with munderficients (TRF) and prophylaxis of diseases or the propertients (TRF) and propertients (TRF) 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39-40; 40pp; English.
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                                                                                                                                                                                                                                                                                                     Burg J,
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q
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The present sequence represents a modified human erythropoietin (BPO)

protein. The EPO was extended at the N-terminal by a proteolytic cleavage

site. It was used to produce conjugates of the invention. The

specification describes a conjugate comprising an EPO glycoprotein having

an N-terminal alpha-amino group, chosen from human EPO (BEPO) or its

analogues (where hEPO is modified by addition of 1-6 glycoprotein is

or a rearrangement of a glycosylation site). The glycosylation sites

or a rearrangement of a glycosylation site). The glycoprotein is

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

bas in vivo biological activity of causing bone marrow cells to increased

circulating half-life and plasma residence time, decreased clearance,

increased clinical activity in vivo, improved potency and stability, when

compared to unmodified EPO. The EPO conjugate is useful for preparing

medicaments for the treatment and prophylaxis of diseases correlated with

anaemia in chronic renal failure patients (CRF), acquired

mundodeficiency syndrome (AIDS) and for treating cancer patients

undergoing chemotherapy. It is also useful for treating patients by

stimulating the division and differentiation of committed erythroid

progenitors in the bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tischer W;
acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schurig HE,
                                                                                                                                                                                              /note= "proteolytic cleavage site"
36. .201
                                                                                                                                                         /note= "secretion signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Engel A, Franze R, Hilger B,
                                                                                                                                                                                                                                       /note= "EPO protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 5; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                         08-DEC-2001; 2001WO-EP014434.
                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-2000; 2000EP-00127891.
                                                                                                                                                                         .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-566640/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL59291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 201 AA;
                                                                                                                                                                                                                                                                               WO200249673-A2.
                                                                                                                                                                           Cleavage-site
                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                    27-JUN-2002
                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burg J,
Wozny M;
                                                                                                                                      Peptide
                                                                                                                                                                                                                   Protein
                                                                                                                        Key
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147 61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120 09 87 88 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLERAL 1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK 28 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK Gaps ; Length 201; Indels Score 861; DB 5; L Pred. No. 1.8e-87; O; Mismatches 5; 96.3**%**; 97.1**%**; Query Match
Best Local Similarity 97.1
Matches 169, Conservative g qq 8 à

121 GAQKEAISPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174 

148

à

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Human, erythropoietin, BPO; glycoprotein; reticulocyte production;
red blood cell production; anaemia; chronic renal failure;
acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
committed erythroid progenitor.
                                                                                          Amino acid sequence of a modified human erythropoietin (EPO)
ABB77899 standard; protein; 169 AA.
                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                    Homo sapiens
                                                              07-0CT-2002
                                                                                                                                                                                                    Synthetic
                              ABB77899;
                                                                                                                                                                                                                                                                                               Protein
   The present sequence is the oligopeptide GST-Epo, which was used in the development of a novel method for increasing the efficiency of gene introduction into a target cell using a retroviral vector. The method comprises carrying out viral infection of the target cell in the presence of a retrovirus and target cell binding substance or substances. The method can be used to effectively introduce genes into target cells for the gene therapy of cancer and viral diseases, e.g. AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 SLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                       GST-Epo; target cell; transfection; retroviral vector; cancer; viral disease; acquired immunodeficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 TKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 TKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 SLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PPR---IEGR-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for increasing efficacy of gene transfer to target cell using retrovirus - by infection of the target cell in the presence of a substance which binds to the virus and a substance which binds to the target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.1%; Score 859; DB 2; Length 412; 93.4%; Pred. No. 8.8e-87; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Koyama N, Hashino K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 146-148; 194pp; Japanese.
                                                AAW33354 standard; protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                         96JP-00051847.
                                                                                                                                                                                                                                                                                                                              96WO-JP003254
                                                                                                                                                                                                                                                                                                                                                           95JP-00294382
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueno T,
                                                                                                                                                                                                                                                                                                                                                                                                        (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                          Oligopeptide GST-Epo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-289294/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Uemori T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT93979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 412 AA;
                                                                                                                                                                     Oligopeptide G
gene therapy;
                                                                                                                                                                                                                                                                                                                              07-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                           13-NOV-1995;
                                                                                                                                                                                                                                                                 WO9718318-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Simi
Matches 171;
                                                                                                             24-FEB-1998
                                                                                                                                                                                                                                                                                              22-MAY-1997
                                                                                                                                                                                                                                  Synthetic.
                                                                              AAW33354;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Asada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                       AIDS
                 RESULT 5
                                   AAW33354
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.3 /note= "proteolytic cleavage site"

Location/Qualifiers

(first entry)

/note= "EPO protein"

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The present sequence represents a modified human erythropoietin (EPO)

protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The clear specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (NEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glyco) group. The EPO glycoprotein covalently linked to a poly(ethylene glyco) group. The EPO glycoprotein site in vivo biological activity of causing bone marrow cells to increase circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified BPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaend in chronic renal failure patients (GRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients or immunodeficiency syndrome (AIDS) and for treating patients by stimulating the division and differentiation of committed erythroid compared in the bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APP-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                        Tischer W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                        Schurig HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 856.5; DB 5
Pred. No. 4.6e-87;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                           Franze R, Hilger B,
                                                                                                                                                                                                                                                           .
نتا
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                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                             08-DEC-2001; 2001WO-EP014434.
                                                                                                                                                                                              20-DEC-2000; 2000EP-00127891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%;
97.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-566640/60.
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                                                                                                                                                                                                                                                                                                                               Engel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 169 AA;
WO200249673-A2
                                                                27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1691
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Best Local S
                                                                                                                                                                                                                                                                                                                                                             Wozny M;
                                                                                                                                                                                                                                                                                                                           Burg J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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GDR 174 GDR 398

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Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
          RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
                                               Human, erythropoietin, EPO, glycoprotein, reticulocyte production,
red blood cell production; anaemia, chronic renal failure,
acquired immunodeficiency syndrome, AIDS; cancer, bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tischer W;
                                    GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                           Amino acid sequence of a modified human erythropoietin (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schurig HE,
                                                                                                                                                                                                                                                                                              "proteolytic cleavage site"
                                                                                                                                                                                                                                                                           "secretion signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                 'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                Hilger
                                                                                                                                                                                                                                                                                                                 note= "EPO protein"
                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                     ABB77902 standard; protein; 196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 40pp; English.
                                                                                                                                                                                                          committed erythroid progenitor.
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                                                                                                                                                                                                                                                                                                                                                                       08-DEC-2001; 2001WO-EP014434
                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-2000; 2000EP-00127891
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Franze
                                                                                                                                                                                                                                                                                     28. .30
/note= "I
                                                                                                                                                                                                                                                                                                        .196
                                                                                                                                                                                                                                                                  1. .27
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                Engel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABL59290
                                                                                                                                                                                                                                                                                                                                  WO200249673-A2
                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                         07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                     27-JUN-2002
                                                                                                                                                                                                                             Synthetic
61
                 99
                                    121
                                                                                                                      ABB77902;
                                                                                                                                                                                                                                                                                                                                                                                                                              Burg J,
Wozny M;
                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                        Protein
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                                                                                            ABB77902
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RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
                                                                                                                                                                                                                                                                                                                   83 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 142
                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human erythropoietin encoded by this sequence is essential for red blood cell formation and is used for the diagnosis and treatment of blood disorders such as anaemia. Large amounts of EPO may be obtained using recombinant DNA techniques in contrast to small amounts obtained from plasma and urine. This sequence is expressed in 8. cerevisiae. See also AANSO346-50 and AAP50299-P50301. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human recombinant erythropoietin expressed in Saccahromyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erythropoietin; red blood cell; erythrocyte; anaemia; blood; disorder;
                                                                                                                                                                                                                                         |||
|----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                               1 APPRIEGRAPPRLICDSRVLERYLLBAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                              Gaps
immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide having properties of erythropoietin - is prepd. by cultivation of transformed eucaryotic or procaryotic host.
                                                                                                                                                                                                                                                                                                                                                                     GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                            5;
                                                                                                                                      Length 196;
                                                                                                                                                                            Indels
                                                                                                                                                                        .0
                                                                                                                                    DB 5;
                                                                                                                                    Score 856.5; DB 5
Pred. No. 5.7e-87;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 82; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP50298 standard; protein; 167
                                                                                                                                    95.8%;
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84US-00582185.
84US-00655841.
84US-00675298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                Query Match
Best Local Similarity 97.1
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIRI ) KIRIN AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1985-159229/26.
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                                                                                                  Sequence 196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-1983;
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01-JAN-1980
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28-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-1985
                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                            143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
  SSSSX8
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                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein chas in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired
                    120
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95.7%; Score 856; DB 1; Length 167; 100.0%; Pred. No. 5.1e-87;

Query Match Best Local Similarity

present sequence represents a modified human erythropoietin (EPO)

The

SEQ ID NO:8

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Matches

89 61 128

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ABU64199 RESULT

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80 VGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 139
                                                                                                                                                                                                                                                                                                                                                   neonatal Fc receptor; central airway epithelium; lung; antigen; tumour antigen; erythropoietin; EPO; growth hormone; interferon-alpha; therapeutic antibode; INF-beta; follicle stimulating hormone; FSH; therapeutic antibody; CAMPATH; SIMULECT; ZENAPAX; REMICADE; HUMIRA; SYNAGIS; RITUXAN; HERCEPTIN; CEA-CIDE; pneumonia; lung cancer; extranodal pulmonary non-Hodgkin's lymphoma; allograft rejection; autoimnume disease; rheumatoid arthritis; Crohn's disease; antirheumatic; antiarthritis; cytostatic; antiinflammatory; immunotherapy; vaccine; human; immunoglobulin G1; IgG1 Fc fragment; Fc-gamma-1; Kb signal peptide; fusion protein; plasmid pED.dC.EpoFc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Systemic delivery of therapeutic agent involves administering effective amount of aerosol of therapeutic agent and neonatal Fc receptor (FCRn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "8 residue peptide linker (SEQ ID NO:27)"
                                                                              .425
e= "BPO/IgG1 Fc fragment fusion protein"
                                                           KEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "IgG1 Fc fragment_(SEQ ID NO:2)"
                                                                                                                                                                                                                                                                                                 Kb signal peptide/EPO/IgG1 Fc fragment fusion protein,
                                                                                                                                                                                                                                                                                                                                      Drug delivery; aerosol; transepithelial; FcRn ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bitonti AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "3 residue peptide linker"
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label= Kb_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Human mature EPO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 8; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simister NE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                        ADO10511 standard; protein; 425 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding partner to lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22. .24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-099348/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADO10510
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                                                                                                                                                                                                                                                                 01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                             AD010511;
                                                                                                 140
                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                      RESULT 10
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                                                                                                                    AVEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an aerosol which comprises a conjugate of a therapeutic agent and neonatal Fc receptor (FcRn) binding partner. The particles in the aerosol have a mass median aerodynamic diameter (MMAD) of at least 3 micro m. The aerosol can be used for the systemic delivery of a therapeutic agent (e.g. antigen (e.g. tumour antigen), polypeptide, oligonucleotide (e.g. antisense oligonucleotide), erythropoietin, growth hormone, interferon-alpha, interferon-beta and follicle stimulating hormone). The present sequence is a protein used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRME
                                             RAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQ
                                                                              1 RAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQ
                                                                                                                                           AVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aerosol useful for systemic delivery of a therapeutic agent e.g. erythropoietin, growth hormone, interferon-alpha, or interferon-beta, comprises a conjugate of the agent and neonatal epithelial receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pED-dC-EpoFc Kbsignal peptide/EPO/Fcgammal insert protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transepithelial systemic delivery; therapeutic delivery; aerosol; FCRn binding partner; lung.
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                                                                                                                                                                                                               SPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 167
                                                                                                                                                                                            SPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bitonti AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 855; DB 7;
Pred. No. 2.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simister NE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sxample 4; Fig 4B; Opp; English.
                                                                                                                                                                                                                                                                                                                          ABU64199 standard; protein; 425
           ô
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 167; Conservative
           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-767442/72.
N-PSDB; AAL56122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003077834-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding partner
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                                                                                                                                                                                                                                                                                                                                                                                                 11-MAR-2004
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             167;
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Synthetic.

The invention relates to a method for the transepithelial systemic

64 VGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 123

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Query Match Best Local Stewart DIH;

Malek LT,

Cossar JD,

WPI; 2004-214326/20.

N-PSDB; ADJ71845

(CANG-) CANGENE CORP

17-JUL-2003; 2003WO-CA001020. 19-JUL-2002; 2002US-0396750P.

WO2004009627-A1

29-JAN-2004

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c delivery of a therapeutic agent. The method involves administering an effective amount of an aerosol of a therapeutic agent (especially an antibody) and a neonatal For teceptor (FCRN) binding partner to the lungs cuch that a central lung zone/peripheral lung zone deposition ratio (C/P ratio) is 0.7 or more. Human FCRN is expressed in adult epithelial tissues, and provides a receptor-specific mechanism for transport across on epithelial barrier. Its expression has been found to be more extensive in central airways than in the periphery of the lung. The invention also relates to an aerosol of a conjugate of a therapeutic agent and an FCRN binding partner, where the aerosol particles have a mass median erodynamic diameter (MMAD) of 3 micrometres or more; an aerosol delivery system; and method for its manufacture. The method can be used to system; and a method for its manufacture. The method can be used to apthelium. Such therapeutic agents include oligonucleotides (including antisense oligonucleotides) or proteins such as antigens (epocially cumour antigens), erythropotetin (EPO), growth hormone, interferon-alpha (IFN-alpha), interferon-beta (IFN-beta), follicle stimulating hormone (FSH) and especially therapeutic or dagnostic antibodies. Therapeutic antibodies that may be administered using the method of the invention may be used to treat deep ung diseases such as RSV pneumonia, cytomegalovirus (CWN) pneumonia, virumity, SYNAGIS, RITUKAN, HERCEPTIN and CEA-CIDE. Therapeutics administered using the method of the invention may be used to treat deep ung diseases such as RSV pneumonia, cytomegalovirus (CWN) pneumonia, cytomegalovirus (CWN) and autoimmune diseases such as such as cancer and allogaraft rejection; and autoimmune diseases chosen from rheumatoid arthritis and cromprising the KPb signal peptide, human EPO and the human IgG1 FC comprising the KP signal peptide, human EPO and the human IgG1 FC comprising the Residual peptide, human EPO and the human IgG1 FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGQQAVEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 VGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-glycosylated EPO analogue with modified protease B signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-glycosylated erythropoietin analogue; EPO analogue; PEG; anaemia;
protease B signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Modified protease B signal peptide region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 KEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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/note= "Non-glycosylated EPO analogue region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 855; DB 8; Length 425;
Pred. No. 2.6e-86;
1; Mismatches 3; Indels
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97.7%;
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Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Unidentified.
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ADJ71846
1D ADJ71846
AC ADJ7184
AC ADJ7184
AX AX DE NOn-
C XX
XX NOn-
C XX
XX C Chim
OS Chim
OS Syncl
OS Syncl
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ET Key
FT Misc
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glycosylated erythropoietin (EPO) analogues, where the lyaine at position 45 and/or 116 has been replaced with an amino acid that cannot be pegylated. The non-glycosylated EPO analogues of the invention are useful for treating anaemia. The present amino acid sequence represents a non-glycosylated EPO analogue with a modified protease B signal peptide. NOTE: The present sequence is included in the sequence listing as SEQ ID No 29, however another sequence on page 28 of the specification is also shown as SEQ ID No 29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A non-glycosylated erythropoietin (EPO) analog useful treating anemia, where the lysine at position 45 and/or 116 has been replaced with an amino acid that cannot be pegylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 AVPTPAAAAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
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small acetyl cholinesterase positive cell; erythrocyte growth effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 GAQKEAISPPDAASAAPLRTITADTFRKUFRVYSNFURGKLKUYTGEACRTGDR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.5%; Score 854; DB 8; L
Best Local Similarity 96.6%; Pred. No. 1.2e-86;
Matches 168; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mega-karyocyte-platelet growth factor; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 29; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of human erythropoietin (EPO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP70398 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86JP-00191542.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 205 AA;
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                                                                                                               All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-platelet growth factor contains human EPO as an active principle. Human EPO has a megakaryocyte colony-stimulating activity and increases the ratio of small acetyl cholinesterase positive cell (SAchE+) which is immature megakaryocyte- Human EPO effects megakaryocyte-platelet system other than an erythrocyte growth effect. Megakaryocyte-platelet growth is usable as a remedy for diseases caused by a platelet decrease
                                                    human
                                                                                                                                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                                                             VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                                                                                                                                                                 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant haematopoietic molecules useful in treating anaemia(s) -comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity.
                                                                                                                                                                                                                                                               9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKEMEVGQQA
                                                                                                                                                                                                                                                                                    APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTRVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                          VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
                                                                                                                                                                                                                                           Gaps
                                                   Megakaryocyte-platelet growth factor - contains as active component erythropoietin and is used to treat diseases caused by decrease in
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                                                                                                                                                                                                                                                                                                                                                              PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166
                                                                                                                                                                                                                      Length 166;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis.
                                                                                                                                                                                                                                                                                                                                                   PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                     95.2%; Score 851; DB 1; I
100.0%; Pred. No. 1.8e-86;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant hematopoietic molecule portion 2.
                                                                                             Disclosure; Page 181; 8pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 32; 82pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 166
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.8
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-150819/18.
                               WPI; 1987-224837/32
           (KAWA/) KAWAKITA M.
                                                                                                                                                                                                  Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ORTH ) ORTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1990;
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                                                                          platelets.
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human erythropoietin (EPO). EPO leads to the maturation of erythrocytes and is therefore designated as a late myeloid differentiation factor (MDF). Within the scope of the invention hybrid molecules were produced which contain at least a portion of an early MDF and at least a portion of a late MDF covalently linked. The EPO sequence given is effective within the scope of the invention in full or in a truncated version.

In an acids 7-161 act as a late MDF when recombined with an early MDF eg. IL-3. These compounds can be used to promote heamatopoiesis in a patient. The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDA to act more specifically to stimulate only the allows the late in the surface of a cell which the early MDF is bound. It also allows the early MDA to act more specifically to stimulate only the useful for treating anaemias of various origins eg. These compounds are useful for treating anaemias of various origins eg.renal failure and ADDS. It is easier to produce and administer one recombinant molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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haematopoietic deficiency; red blood cell; erythroid progenitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 851; DB 2; Length 166; Pred. No. 1.8e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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N-PSDB; AAV31031.
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optionally 1-6 amino acids from the N-terminus and 1-5 from the C-terminus can be deleted, (b) the N-terminus is joined to the C-terminus directly or through a linker (see AAW89405-12) capable of joining the N-terminus to the C-terminus, (c) there are new C- and N-termini at any two consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42, 43-44 to 48-49, 50-51 to 57-58, 77-78 to 82-83, 84-85 to 88-89, and 108-109 to 131-132, and (d) optionally the agonist polypeptide is preceded by Met, Ala, or Met-Ala. 60 of these circularly permuted EPO receptor agonists (see AAW58413-72) are claimed. Also claimed are: nucleic acid molecules (see AAW58413-72) are claimed. Also claimed are: nucleic acid method of producing an EPO receptor agonist using transfected host cells; and methods for stimulating the production of haematopoietic cells, for selective ex vivo expansion of erythrosid progenitors, and treating patients having a haematopoietic disorder using the BPO receptor agonists. The RPO recent agonists the PPO recent agonists. the EPO receptor agonists. The EPO receptor agonists retain one or more activities of native EPO and may also show improved haematopoietic cellstimulating activity and/or an improved activity profile which may include reduction of undesirable biological activities associated with native EPO and/or have improved physical properties such as increased solubility, stability and refold efficiency Sequence 166 AA; 

VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128 61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120 9 9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA ö PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166 Length 166; Indels 95.2%; Score 851; DB 2; 100.0%; Pred. No. 1.8e-86; 0; Mismatches Conservative Local Similarity 166; 69 129 Query Match Matches 셤 ò g à à g

AAW77780 standard; protein; 166 AA.

AAW77780;

(first entry) 24-NOV-1998 Human BPO receptor agonist polypeptide.

Haematopoietic receptor agonist, erythropoietin receptor agonist, BPO, human; chimeric protein; stem cell expansion; tumour; infection; autoimmune disease; haematopoietic disorder; therapy; dendritic cell.

sapiens Ношо

note= "1-6 amino acids of the N-terminus are optionally ote= "possible positions of new C- and N-termini" new C- and N-termini" "possible positions of new C- and N-termini" new C- and N-termini" C- and N-termini" C- and 24..25 /note= "possible positions of new 25. .26 / /note= "possible positions of new 'note= "possible positions of "possible positions of Location/Qualifiers deleted" Misc-difference 28. .29 Misc-difference 29. .30 . 24 note= /note= 'note= Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference 

70. 51
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71. 52
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52. 53
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23-OCT-1997;
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//note= "possible positions of new C- and N-termini"

ce 124. .125

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ce 125. .126

//note= "possible positions of new C- and N-termini"

ce 126. .127

//note= "possible positions of new C- and N-termini"

ce 126. .127

//note= "possible positions of new C- and N-termini"

ce 126. .129

//note= "possible positions of new C- and N-termini"

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WO9817810-A2

30-APR-1998

96US-0029629P 25-OCT-1996;

97WO-US020037.

(SEAR ) SEARLE & CO G D.

Staten NR; earn JP, Summers NL, S' Minster NI, Woulfe SL; Feng Y, Mckearn JP, Minnerly JC, Minster CA, Streeter PR, Mcwherter

NPI; 1998-261504/23.

Multi-functional chimeric haematopoietic receptor agonist - useful to treat haematopoietic disorders, tumours, infections or autoimmune

A human erythropoietin (EPO) receptor agonist polypeptide comprises a modified EPO amino acid sequence of the formula provided in AAW7780, in which the N-terminus is joined to the C-terminus directly or via a linker, the polypeptide having new C- and N-termini at one of the constitutions indicated. Novel claimed multi-functional chimeric beamatopoietic receptor agonists (see AAW77812-22) have the formula R1-L1 erg. R2. R2.11-R1. R1-R2 or R2-R1, where L is a linker and R1 and R2 are independently selected from: (a) the human EPO receptor agonist; (b) a human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a modified constitution factor (G-CSF) polypeptide (see AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784); (c) modified human interleukin-3 polypeptide (see AAW77784); (c) modified human interleukin-3 polypeptide (see AAW77784); (c) modified human consisting of a CSF, a cytokine, a factor selected from the group consisting of a CSF, a cytokine, a consisting and polypeptide (see AAW77785); (d) modified human at least R1 or R2 is selected from (a), (b) or (c) as above. The consisting of a tleast R1 or R2 is selected from (a), (b) or (c) as above. The consisting consisting of a consisting consisting of a consisting consi 1 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDIKVNFYAWKRMEVGQQA APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 0 Score 851; DB 2; Length 166; Pred. No. 1.8e-86; 0; Indels 95.2%; Scor. 100.0%; Pred. No. ... 0; Mismatches Claim 1; Page 762; 841pp; English. Query Match 95.2 Best Local Similarity 100. Matches 166; Conservative diseases g ò

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69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128 

Search completed: November 19, 2004, 21:05:44 Job time : 64.2534 secs

PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166

PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174

129 121

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JPPLICANI: COUNTY, Takashi
Uemo, Takashi
Ueno, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: «Unknown:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-007-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: <Unknown>
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APPLICANT: Asada, Kiyozo
Uemori, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Philadelphia STATE: PA
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Sequence 2, Appli
Sequence 2, Appli
Sequence 37, Appl
Sequence 14, Appli
Sequence 14, Appli
Sequence 1, Appli
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Sequence 34, Appl
                                                                                         November 19, 2004, 21:00:09; Search time 17.8375 Seconds (without alignments) 646.913 Million cell updates/sec
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Sequence 46,
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-809-156B-34
US-08-809-156B-34
US-09-604-871-2
US-09-604-938-2
US-09-462-941-2
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US-08-938-2
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US-09-604-871-1
US-09-552-265B-5
US-09-552-265B-5
US-09-552-265B-30
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US-09-552-265B-24
US-09-552-265B-36
US-09-552-265B-40
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                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                          US-10-014-363-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                       Searched:
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                                                                                              on:
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87	826	92.4	166	4	US-09-552-265B-26	
29	826	92.4	166	4	US-09-552-265B-31	31,
30	826	92.4	193	4	US-09-552-265B-42	42,
31	826	92.4	193	4	US-09-552-265B-47	47,
32	825	92.3	166	4	US-09-552-265B-18	18,
33	825	92.3	166	4	US-09-552-265B-23	23,
34	825	92.3	166	4	US-09-552-265B-28	28,
35	825	92.3	166	4	US-09-552-265B-33	33,
36	825	92.3	193	4	US-09-552-265B-34	34,
37	825	92.3	193	4	US-09-552-265B-39	39,
38	825	92.3	193	4	US-09-552-265B-44	44
39	825	92.3	193	4	US-09-552-265B-49	49,
40	823	92.1	166	4	US-09-552-265B-21	21,
41	823	92.1	166	4	US-09-552-265B-25	25,
42	823	92.1	193	4	US-09-552-265B-37	37,
43	823	92.1	193	4	US-09-552-265B-41	41.
44	822	91.9	166	4	US-09-552-265B-27	27.
45	822	91.9	193	4	US-09-552-265B-43	
					ALIGNMENTS	

Gaps

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336 SLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRT 395
                                                                                                                                                                                                                                                                                                                                                                                       52 TKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 SLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 70, Application US/08318193
Patent No. 5641663
Patent No. 5641663
Patent No. 5641663
APPLICANT: GARVIN, Robert T.
APPLICANT: MALEK, Lawrence T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
TITLE OF INVENTION: SIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCES: Poley & Lardner
                                                                                                                                                                                                                                                                                  2 PPR---IEGR-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPD
                                                                                                                                                                             Score 859; DB 4; Length 412; Pred. No. 1.1e-99; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/318,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
RATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
RECISTRATION NUMBER: 18740/116 CACO
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELERAX: (703)836-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 166 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PULDA PELICATION DATA:
APPLICATION NUMBER: US/07/935,314
                                                                                                                                                                               Query Match
Best Local Similarity 93.4%;
Matches 171; Conservative
LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                               TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-809-156B-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
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COUNTRY: USA
ZIP: 22313-0299
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US-08-318-193-70
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                                                                                                                                                                                                                                                                                                                                               276 TKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 335
                                                                                                                                                                                                                                                                                                                                                                                                                     112 SLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRŢ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PPR---IEGR-----APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPD
                                                                                                                                                               Gaps
                                                                                                                                                             10;
                                                                                                          Length 412;
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                                                                                                                                                             Indels
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STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMEN PC-DOS/MS-DOS
SOFTWARE: PATEMEN PC-DOS/MS-DOS
SOFTWARE: PATEMEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-MOV-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-MOV-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: TO 051847/1996
APPLICATION NUMBER: TO 051847/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Uemori, Takashi
APPLICANT: Uemori, Takashi
APPLICANT: Uemori, Takashi
APPLICANT: Woyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO
TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CONTROLLY: Philadelphia
                                                                                                       Query Match 96.1%; Score 859; DB 4; Best Local Similarity 93.4%; Pred. No. 1.1e-99; Matches 171; Conservative 2; Mismatches 0.
       ; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Weiser, Gerard J.
REGISTRATION UNUMBER: 19,763
REFRENCE/DOCKET NUMBER: 977.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEPAX: 215-875-8384
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDR 174
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RESULT 7
PCT-US94-04361-37
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US-09-462-941-2
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                                                                                                                                                                                                SEQ ID NO 2
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                                                                                                                                                                                                                                   69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                                                                    1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 60
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                                                                                                                                 9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                Length 166;
                                                                                                                                                                                                                                                                                          129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
95.2%; Score 851; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 166; Conservative 0; Mismatches 0; Indels
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                                                                                                 0; Indels
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                                                        Score 851; DB 1; I
Pred. No. 2.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Higger, Berne
APPLICANT: Higger, Berne
TITLE OF INVENTION: EXYTHROPOLETIN CONJUGATES
FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 1999-08-30
PRIOR PILING DATE: 1999-08-30
PRIOR PILING DATE: 1999-08-05
PRIOR PELICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/147,452
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATCHTIN VET: 2.1
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Patent No. 6583272
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION:
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
                                                    Query Match
95.2%; Score 851; DB
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 166; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09604871; Patent No. 6340742
protein
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ORGANISM: Homo sapiens
MOLECULE TYPE:
  ; MOLECULE 111
US-08-318-193-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
LENGTH: 166
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US-09-604-938-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 1997-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 166;
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Pred. No. 2.6e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                         95.2%; Score 851; DB 4; 100.0%; Pred. No. 2.6e-99; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.2%; Score 851; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 166; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR FILING DATE: 1999-10-17
PRIOR PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR PELLING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR ELLING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/09462941
; Patent No. 6668183
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 166; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-604-938-2
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ORGANISM: Homo sapiens
US-07-903-220-1
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                                                                                          New York
                                                                                                                       USA
                                                                                  STATE: New COUNTRY: USZIP: 10004
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Patent No. 5322837

GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: BEYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
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APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Bunn, MA 02115
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyi
APPLICANT: Wen, Danyi
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Expthropoietin Muteins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne "STERME STERME STE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 PPDAASAAPLRTITADIFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
COUNTY: U.S.A.
ZIP: 20005-1934
COMPUTER READABLE FORM:
COMPUTER: READABLE FORM: PC COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:

APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336
TELEPHONE: (202) 371-260
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 166 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 166; Conservative
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69 VEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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Sequence 34, Application US/08883795A

Sequence 34, Application US/08883795A

Sequence 34, Application US/08883795A

Patent No. 59856A

APPLICANT: Manag, Gregor

APPLICANT: Manag, Gregor

TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator

TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator

CORRESPONDENCE ADDRESS:

ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
CITY: Toronto
STATE: Ontario
COMTRY: Canada
ZIP: MSH 3YZ
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.2%; Score 851; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.3e-99;
Matches 166; Conservative 0; Mismatches 0;
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LENGTH: 165
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APPLICANT: DeSauvage, Frederick
APPLICANT: Henner, Dennis, J.

ITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypeptides and nucleic acids encoding the same FILE REFERENCE: GENENT.057CPl
CURRENT APPLICATION NUMBER: uS/09/552,265B
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: uS 09/307307
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 193
ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
TELEPHONE: (416) 364-7311
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09552265B Patent No. 6555343
                                                                                                                                                                                                              : 193 amino acids
amino acid
                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-883-795A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-265B-4
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US-09-552-265B-4
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APPRLICDSRVLERYLLBAKBAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 94.6%; Score 846; DB 3; Length 165; Best Local Similarity 100.0%; Pred. No. 1.1e-98; Matches 165; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRIGD 165
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100.0%; Pred. No. 1.1e-98;
tive 0; Mismatches 0;
                                                                    APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Hilger, Bernd
APPLICANT: Holger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: EXYTHOPOIETIN CONJUGATES
FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR PILING DATE: 1999-08-06
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 1097 nonprovisional CURRENT APPLICATION NUMBER: US/09/604,938 CURRENT FILING DATE: 2000-06-27 PRIOR APPLICATION NUMBER: 60/166,151 PRIOR FILING DATE: 1999-10-17 PRIOR FILING DATE: 1999-08-13 PRIOR FILING DATE: 1999-08-23 PRIOR FILING DATE: 1999-08-23 PRIOR FILING DATE: 1999-08-23 PRIOR FILING DATE: 1999-07-02 NUMBER OF SEQ ID NOS: 3 SECTRARE: Patentin Ver: 2.1 SEQ ID NO 1
Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-604-938-1
; Sequence 1, Application US/09604938
; Patent No. 6583272
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 165; Conserva
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88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 147
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Patent No. 6555343
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: NO. 6555349el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: NO. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: NO. 6555349el chimpanzee
FILLE REPERENCE: GENERAL OF CO. 6555349el chimpanzee
TITLE OF INVENTION: NO. 6
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Pred. No. 2.7e-98;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.3%; Score 843; DB 4; Length 193; 99.4%; Pred. No. 3.4e-98; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                                                           APPLICATION NUMBER: US/09/554,451
FILING DATE: 15-May-2000
CLASSIFICATION: <unbox/doi/10.0000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/03449
FILING DATE: No. 6680207ember 16, 1998
APPLICATION NUMBER: GB 9723955.2
FILING DATE: No. 6680207ember 14, 1997
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.4%;
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.3
Best Local Similarity 99.4
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-554-451-8
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APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc.

APPLICANT: Carcogno, Carlos Miguel

APPLICANT: Carcogno, Carlos Miguel

APPLICANT: Carcogno, Carlos Miguel

APPLICANT: Melo, Carlos Applicant: Melo, Carlos Applicant: Welo, Carlos Carlos
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                                                                                                                                         VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                       61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
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1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 60
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                                                                                                                                                                                                                                                                                                              129 PPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGD 173
                                                                                                                                                                                                                                                                                                                                                                     121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 165
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TITLE OF INVENTION: Detection of Molecules in Samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.6%; Score 846; DB 4; I
100.0%; Pred. No. 1.1e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09554451
Patent No. 6680207
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09830967
Patent No. 6777205
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 165
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Matches 165; Conservative
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US-09-830-967-1
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US-09-554-451-8
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US-09-830-967-1
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Search completed: November 19, 2004, 21:13:01 Job time : 18.8375 secs

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November 19, 2004, 21:11:10 ; Search time 82.4565 Seconds (without alignments) 747.281 Million cell updates/sec
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1. Cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US07 WIRW PUB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

1. Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2. Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2. Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

2. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

2. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

2. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

3. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

4. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

5. Cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*

6. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

7. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

8. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

9. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

9. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

9. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

9. Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1570615 segs, 354127592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
                                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Description	Segment	Segmence 5 Appli	Segmence 34	Segment	Cret FeS	Sedimen		Crat Feb.	Seamon	Seamon	Segmen	Segmen	Sequence 2, Appli
				63-3	63-5	64-34	63-4	8-80	08-8	1-2	63-2	56-2	51-2	77-2	08-2	48-2
SUMMARIES				014-3	014-3	775-9	014-3	435-6	622-1	53-73	014-3	241-3	293-5	400-3	400-7	298-1
_			ID	US-10-	US-10-	-60-SU	US-10-	US-10-	US-10-	NS-09-8	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-298-148-2
			DB	13	13	10	13	14	15	6	13	14	14	14	14	14
			core Match Length DB I	174	174	412	169	425	425	166	166	166	166	166	166	166
	₩	Query	Match	100.0	96.3	96.1	95.8	95.6	95.6	95.2	95.2	95.2	95.2	95.2	95.2	95.2
			Score	894	861	859	856.5	855	855	851	851	851	851	851	851	851
		Result	No.	н	7	m	4	S	9	7	80	6	10	11	12	13

0

0; Gaps

100.0%; Score 894; DB 13; Length 174; 100.0%; Pred. No. 3.8e-90; ive 0; Mismatches 0; Indels 0.

Query Match
Best Local Similarity 100.
Matches 174; Conservative

8 6 8 6

; SEQ ID NO 3 ; LENGTH: 174 ; TYPE: PRT ; ORGANISM: CHO/dhfr-US-10-014-363-3 09

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ω	1	. 2	166	15	8-10-467-115-1	Sequence 1, Appli
æ	6	. 2	166	16	-10-658-8	equence
80	1	.2	166	16	US-10-773-939-2	egnence
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80	1 9	2.	166	16	-10-468-496	equence 13.
80	1 9		9	17	-10-773-654-2	ا د
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80	6	2	193	17	US-10-676-694-10	,
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00	6		163	17	IIS-10-676-694-112	- 0
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	o,	6.	193	16	-10-612	64
	~		193	16	US-10-612-665-70	7.0
	_	6.	193	16	-10-612-665-8	α
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					ALIGNMENTS	
RESULT 1						
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; Sequence 3,		catio	Application US/1001436	0014	363	
; Publication	No. U	82002	No. US20020115833A1	3A1		
; GENERAL INFORMATION	ORMATI	oN:				
; APPLICANT:			Į.			
; APPLICANT:	Engel,		Alfred			
, APPLICANT:	Franze,		Reinhard	Ġ		
; APPLICANT:		er, B	Bernd			
, APPLICANT:	Schurig,	rıg,	Hartmut		Ernst	
, APPLICANT:		ner,	Wilhelm	E		
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. FILE PERFPRICE. Case 2000s	PNCE.		20005	TOT TOT	can conjugaces	
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TIRBENT FI	FILING DATE	NOT A	OMBEK:	: US/1	10/014,363	
, F	SEO ID	NON	4 L	J	-	
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216 PPKSDLIEGRGIPRNSGAPPRLICDSRVLQRYLLEAKEAENITIGCAEHCSLNENITVPD 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLITILIRALGAQKEAISPPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PPR---IEGR-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.1%; Score 859; DB 10; 93.4%; Pred. No. 9.1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Burg, Josef
APPLICANT: Brigel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Franze, Reinhard
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT FILING AND NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                         PRIOR AFFLOATION NUMBER: US/09/366,009
FILING DATE: U2-Aug-1999
APPLICATION NUMBER: 08/809,156
FILING DATE: «Unknown»
APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: UP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-775-964-34
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                        <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10014363; Publication No. US20020115833A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
                FILING DATE: 20-Feb-200:
CLASSIFICATION: <Unknow
                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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ORGANISM: CHO/dhfr-
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LENGTH: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNF1RGKLKLYTGEACRTGDR 174
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Publication No. US20030087437A1
GENERAL INFORMATION:
APPLICANT: Aada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, No. US20030087437Aluto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: BETHOOVIRUS
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 861; DB 13; Length 174;
Pred. No. 1.7e-86;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19102
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
                                                                                                                                                                                                                                                                        APPLICANT: Franze, Reinhard
APPLICANT: Hilder, Bernd
APPLICANT: Hilder, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Worder, Wilhelm
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                           Sequence 5, Application US/10014363 Publication No. US20020115833A1 GENERAL INFORMATION APPLICANT: Burg, Josef APPLICANT: Engel, Alfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin version 3.1; SEQ ID NO 5; LENGTH: 174; TYPE: PRT 7 CHO/dhfr-US-10-014-363-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.1;
Matches 169; Conservative
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-10-014-363-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                           20 RAGSRAPPRLICDSRVLQRYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRME 79
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                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                 Score 855; DB 15;
Pred. No. 2.6e-85;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-853-731-2
Sequence 2, Application US/09853731
Patent No. US20020037841A1
GENERAL INFORMATION:
TITLE OF INVENTION: Erythropoietin Composition
TITLE OF INVENTION: Erythropoietin Composition
FILE REFERENCE: 20619 US
CURRENT APPLICATION NUMBER: US/09/853,731
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP/00110355.5
PRIOR FILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 851; DB 9;
Pred. No. 2e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.2%; Scc. 100.0%; Pred. No. 2. ... 0; Mismatches ... 0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US02/21355
PRIOR FILING DATE: 2002-07-03
PRIOR PPLICATION NUMBER: US 60/364,482
PRIOR FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NO 8
LENGTH: 425
TYPE: PRT
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Best Local Similarity 97.7%;
Matches 167; Conservative
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APPLICANT: Engel, Alfred
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ORGANISM: Homo sapiens
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Best Local Similarity
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Publication No. US20030235536A1
GENERAL INFORMATION:
APPLICANT: Blumberg, Richard S.
APPLICANT: Lencer, Wayne I.
APPLICANT: Lencer, Wayne I.
APPLICANT: Blumberg, Richard AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTI
FILE REFERENCE: SO133.70010.US
CURRENT APPLICATION NUMBER: US/10/435,608
CURRENT FILING DATE: 2003-05-09
CURRENT FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
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Publication No. US20040063912A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blumberg, Richard S.
APPLICANT: Blumberg, Richard S.
APPLICANT: Blumberg, Richard I.
APPLICANT: Binchti, Alan J.
TITLE OF INVENTION: CENTRAL AIRWAY ADMINISTRATION FOR SYSTEMIC DELIVERY OF THERAPEUTI FILE REFERENCE: S01383.70011.US
CURRENT APPLICATION NUMBER: US/10/622,108
CURRENT FILING DATE: 2003-07-17
PRIOR FILING DATE: 2003-05-09
PRIOR FILING DATE: 2003-05-09
                                                                                                                                                                                                                    56 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 115
                                                                                                                                                                                         61 RMEVGOQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
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                                                                                                                              1 APP----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK 55
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                                                                                                     1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
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                  Score 856.5; DB 13;
Pred. No. 5e-86;
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Pred. No. 2.6e-85;
1; Mismatches 3;
95.8%; Sco...
97.1%; Pred. No. co...
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Best Local Similarity 97.7%;
Matches 167; Conservative
                                    Best Local Similarity 97.1
Matches 169; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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                    Query Match
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Sequence 2, Application US/10293551
Publication No. US20030120045A1
GANERAL INFORMATION
APLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REPERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/29,551
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/604,938
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR APPLICATION NUMBER: 60/16,154
PRIOR APPLICATION NUMBER: 60/15,548
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
PRIOR FILING DATE: 1999-08-23
NUMBER: OF SEO ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 100.
Matches 166; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 166
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Sequence 2, Application US/10241356

Publication No. US20030077753A1

GENERAL INFORMATION:
APPLICANT: TISCHER, WILHELM
TITLE OF INVENTION:
FILE REFERENCE: 2091
CURRENT APPLICATION NUMBER: US/10/241,356
CURRENT FILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: EP 01122555.4

PRIOR FILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTI Ver. 2.1
                                APPLICANT: Hilger, Bernd
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 166
               Franze, Reinhard
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Matches 166; Conservative
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, ORGANISM: Homo sapiens
US-10-014-363-2
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APPLICANT:
APPLICANT:
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                                                                                                               9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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APPLICANT: Bolder Biotechnology, Inc.
ITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/400,377
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR APPLICATION NUMBER: 60/052,516
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTING DATE: 1997-07-14
SOFTWARE: PATENTING DATE: 2.0
SEQ ID NOS: 41
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95.2%; Score 851; DB 14; Length 166; 100.0%; Pred. No. 2e-85; ive 0; Mismatches 0; Indels
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                          VEVWQGLALLSBAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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**Fublication No. US2030171284A1

**GENERAL INFORMATION:

**APPLICANT: COX III, George N

**APPLICANT: Bolder Biotechnology, Inc.

**TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

**TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

**TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

**TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

**TITLE OF INVENTION: UNMBER: US/09/462,941

**PRIOR APPLICATION NUMBER: US/09/462,941

**PRIOR PILING DATE: 2000-11-4

**PRIOR PILING DATE: 1997-07-14

**NUMBER OF SEQ ID NOS: 41

**SEQ ID NOS: 41
                                                                                                                                                                                                                        Sequence 2, Application US/10400708
Publication No. US20030166865A1
GENERAL INFORMATION:
APPLICANT: Cox III, George N
TITLE OF INVENTION:
FILE REFERENCE: 4152-1-PUS
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR APPLICATION NUMBER: 60/052,516
PRIOR FILING DATE: 2000-01-14
SPRIOR RILING DATE: 2000-01-14
SPRIOR FILING DATE: 2000-01-14
SPRIOR FILING DATE: 2000-01-14
SPRIOR SEQIENCE: 1997-07-14
SPRIOR FILING DATE: 1997-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                         129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo sapiens
US-10-400-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Homo sapiens
US-10-298-148-2
                                                                                                                                                                                     RESULT 12
US-10-400-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 166
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US-10-298-148-2
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Sequence 227, Application US/10360101
Sequence 227, Application US/10360101
Publication No. US20040009550A1
GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantiblotic way;
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
FILE REFERENCE: 2003-02-07
FILE REFERENCE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Parentin version 3.1
SEQ ID NO 227
LENGTH: 166
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                                                                                                   9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                              Gaps
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                                                         0;
     95.2%; Score 851; DB 14; Length 166;
100.0%; Pred. No. 2e-85;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 166;
                                                                                                                                                                                                                                                                                                                                    129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10467115
; Publication No. US20040063917A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carrer, Graham
; APPLICANT: Alliams, Stephen
; TITLE OF INVENTION: MODIFIED ERYTHROPOLETIN (EPO) WITH
; FILE OF INVENTION: REDUCED IMMUNOGENICITY
; FILE REFERENCE: MER.114
; CURRENT APPLICATION NUMBER: US/10/467,115
; CURRENT APPLICATION NUMBER: 01102615.0
; PRIOR FILING DATE: 2001-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
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95.2%; Score 851; DB 15;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: sequence of erythropoietin
US-10-360-101-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 100.0
Matches 166; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 19, 2004, 20:59:24; Search time 20.1934 Seconds (without alignments) 829.068 Million cell updates/sec Run on:

894

1 APPRIEGRAPPRLICDSRVL.....NFLRGKLKLYTGEACRTGDR 174 US-10-014-363-3 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SIMMARIES

		Description	ervthropoietin pre						DI	4 1	1	ervthropoietin - d	he	thrombopoietin - h	thrombopoietin pre		Solute binding rec		megakarvocyte grow	UDP-N-acetylpyruvo	probable 2-hydroxy		ਾਹ	genome polyprotein	ribosomal protein	probable sensory h	a	transport		methylamine utiliz	probable copper-tr
SUMMARIES		ID	ZUHU	JQ0173	I84613	146083	S28148	I46401	A24902	JC7699	I46578	146199	AF0526	G02729	I80105	AB0323	AE0959	D64738	A55530	A83274	A10443	H85498	H90647	GNWVJ8	S56639	T35681	A54696	T35450	AG2919	H97693	S36741
		B :	Н	П	Н	П	П	7	7	~	Ŋ	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	N	7	Ŋ	7
		Length	193	192	192	188	192	194	192	195	190	175	813	353	353	323	346	824	286	339	296	824	824	3033	480	1829	897	348	455	455	747
٠	Query	Match		•	•		79.0			76.7	76.4										•			9.1				8.7		٠.	8.7
		Score	851	69	764.5	718	_	690.5	9	685.5	683	638	91.5	06	89	88	87.5	7	86		m	N	$^{\circ}$	81.5	σ	σ	78.5	78	78	78	78
	Result	No.	7	N	m	4	3	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	60 kD chaperonin [	symbionin syml, -	bacterioferritin X	mandelate racemase	groEL protein - Ba	hypothetical prote	hypothetical prote	conserved hypothet	rts beta (AF305057	sensor/response re	RF2 protein - saim	thrombonoietin nre	ribonucleoside-dip
AD1928	875569	828798	B84932	B42281	H82810	AE3465	837039	875772	E84310	AB2922	C97696	E83529	B37994	JC4125	AH3625
7	7	0	0	~	N	7	~	N	~	~	~	~	7	7	7
242	451	388	548	548	154	425	544	637	300	400	425	925	282	326	335
8.7	8.7	9.8	9.8	9.8	9.8	9.6	8.4	8.4	8.3	8.3	8.3	8.3	8.3	8.3	8.3
77.5	77.5	77	77	77	76.5	76.5	75.5	75.5	74.5	74.5	74.5	74.5	74	74	74

#### ALIGNMENTS

RESU ZUHU eryt	RESULT 1 2UHU 2Ythropoietin precursor [validated] - human C.Smeries: Homo canions (man)
O O O C Z	C.pspcress nono saptens (man) C.Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004 C.Accession: A01855, A24744; A25384; A22210; S56178 K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, A06-810, 1985
A,TR	A.Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet A.Reference number: A01855; WUID:85137899; PMID:3838366 A.Accession: A01855
A;R	A;Molecule type: mRNa; DNA A;Residues: 1-193 <jac></jac>
A;C R;L	A;Cross-references: UNIPROT:P01588; GB:X02157; GB:X02158 R;Lin, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.;
Pro A;T	etin gene.
A;A	A;Kereronce number: A24/44; MUID:8606/948; PMID:3865178 A;Accession: A24744
E K	A;Molecule type: DNA A:Residues: 1-193 <lin></lin>
A t	A, Cross-references: GB:M11319; NID:g182197; PIDN. AAA52400.1; PID:g182198
4 ·	Kjudi, F.H.; Everett, K.; Mang, F.F.; Arakawa, T.; Goldwasser, E. J. Biol. Chem. 261, 3116-3121, 1986
A; A	A:Title: Structural characterization of human erythropoietin. A:Reference number: 055384. Mith.0514000. DMTD.304005
A;A	A:Accession: A2238
A; A	A; Wolecule type: protein
A E	A;Experimental source: urine
N, A	A, Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid
Д.	R;Yanagawa, S.; Hirade, K.; Ohnota, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M. J. Biol. Chem. 259, 2707-2710, 1984
A; T	itle: Isolation of human erythropoietin with monoclonal antibodies.
A;A	A;Reterence number: A22210; MUID:84135751; PMID:6698989 A;Accession: A22210
A; W	olecule type: protein
A A	esidues: 28-29,'X',31-33,'L',35-50,'X',52-53,'D',55,'G',57 <yan> atsumoto, S.; Ikura, K.; Ueda, M.; Sasaki, R.</yan>
Pla	nt Mol. Biol. 27, 1163-1172, 1995
A A	A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured A;Reference number: \$56178; MUID:95284365; PMID:7766897
A;A	A;Accession: S56178
A; A	A;Molecule type: protein A;Residues: 28-33.'X'.35-37 <mts></mts>
Ü	C; Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
5 €.	C;Genetics: A;Gene: GDB:EPO
e e	A;Cross-references: GDB:119110; OMIM:133170
A C	A; Introns: 5/1; 53/3; 82/3; 142/3
	C;Function:

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R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Exythropoietin structure-function relationships: High degree of sequence homolo A;Reference number: 146083; MUID:93372347; PMID:8364201
A;Accession: 184613
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Preliminary; A;Reference number: A;Residues; 1-192 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q28513; GB:L10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 193
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolc
A;Reference number: 146083; MUID:93372347; PMID:8364201
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A,Residues: 1-188 (wRNs)
A,Cross-references: UNIPROT:P33708, GB:L10606; NID:g163820; PIDN:AAA30807.1; PID:g163821
C,Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of c,Function:
A,Description: the primary inducer of erythrocyte formation
G,Superfamily: erythropoietin
C,Keywords: erythropoietin; hormone; kidney; liver
F,1-22/Domain: signal sequence (fragment) #status predicted (*SIG>
F,23-188/Product: erythropoietin #status predicted (*MAT>
F,22-183/F):uslfide bonds: #status predicted
F,46,60,105/Binding site: carbohydrate (Ser) (covalent) #status predicted
F,148/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: I46083
                                      change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 APPRLICDSRVLERYILEAREAENVINGCAEGCSFSENITVPDIKVNFYTWKRMDVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 APPRLVCDSRVLERYLLEAKEAENVTWGCSESCSLNENITVPDTKVNFYAWKRIEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: erythropoietin
C; Superfamily: erythropoietin
C; Reywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F; 1-27/Domain: signal sequence #status predicted <515.
F; 28-192/Product: erythropoietin #status predicted <AMI>
F; 28-192/Product is erythropoietin #status predicted <F; 55-60/Disulfide bonds: #status predicted <F; 51.65, 110/Binding site: carbohydrate (Asn) (covalent) #status predicted F; 152/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 LPDAASAAPLRTITADTFCKLFRVYSNFLRGKIKLYTGEACRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 718; DB 1; Length 188;
Pred. No. 1.7e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Description: the primary inducer of erythrocyte formation
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_
C;Accession: 184613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
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A;Molecule type: mRNA
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Cipacession: 07-2014

Cipacession: 07-2017

Rilin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Cgene 44, 201-209, 1986

A; Title: Monkey erythropoietin gene: cloning, expression and comparison with the human expression: 070173

A; Reference number: 070173; MUID:87055236; PMID:2877922

A; Reference number: 070173; MUID:87055236; PMID:2877922

A; Residues: 1-192 «LIN»

A; Residues: 100 «Lindies «Lin»

B; Residues: 100 «Lindies »

B; Residues: 100 «Lindies »

B; Residues: 100 «Lindies »

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                    (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .Species: Macaca fascicularis (crab-eating macaque)
.Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTKVNFYAWKRMEVOQQA
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       A,Description: the primary inducer of erythrocyte formation C;Superfamily: erythropoletin C;Keywords: erythropoletin C;Keywords: erythropoletis; glycoprotein; hormone; kidney; liver F;1-27/Domain: signal sequence #status predicted <SIG> F;28-193/Product: erythropoletin #status experimental <MAT> F;34-188,56-60/Disulfide bonds: #sratus experimental F;31.65,110/Binding site: carbohydrate (Ser) (covalent) #status experimental F;51.65,110/Binding site: carbohydrate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 193
                                                                                                                                                                                                                                                                                                                                                    Score 851; DB 1; Length 193
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                                                                                                                                                                                                                                                                                                                                            Query Match 95.2%; Score 851; Db 1; 1
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 166; Conservative 0; Mismatches 0;
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Pred. No. 2.3e-65;
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91.6%;
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A;Reference number: 146083; MUID:93372347; PMID:8364201
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A;Molecule type: mRNA
A;Residues: 4-15,'L',17-107,'P',109-194 <WEN>
A;Residues: 4-15,'L',17-107,'P',109-194 <WEN>
CCOMBELEFERENCES: GB:L10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c;Punction:
                                 Cross-references: UNIPROT: P33709; EMBL: Z24681; NID: 9395049; PIDN: CAA80848.1; PID: 93950
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A; Residues: 1-192 <br/>
A; Cross-references: UNIPROT: P07321
A; Cross-references: UNIPROT: P07321
A; Molecule type: DNA
A; Cross-references: Universe translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
B; McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A; Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A; Reference number: A24901; MUID: 87039104; PMID: 3022133
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C;Comment: Brythropoietin is produced by Kidney or liver of adult mammals and by liver o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and human gene homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 APPRLICDSRVLERYILEAREAENATMGCAEGCSFSENITVPDTKVNFYAWKRMEVQQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: the primary inducer of erythrocyte formation (superfamily: erythropoietin
(Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone, kidney; liver
C;Keywords: erythropoietin #status predicted (sIG»
F;18-194/Product: erythropoietin #status predicted (AMI)
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;154/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 LPDATPSAAPLRIFTVDALSKLFRIYSNFLRGKLTLYTGEACRRGDR
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Pred. No. 6.9e-58;
9; Mismatches 20
                                                              R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
77.2%;
Best Local Similarity 82.0%;
Matches 137; Conservative
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A;Residues: 1-67,'P',69-192 <MCD>
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A;Residues: 1-194 <FUX>
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C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C:Accession: S28148; IG5743
R;Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
B;Onsya, A.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
B;Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R.
A;Title: Nucleotide sequence of rat erythropoietin.
A;Reference number: S28148; MUID:93042015; PMID:1420369
A;Accession: S28148
A;Molecule type: mRNA
A;Residues: 1-192 <ANGA>
A;Cross-references: UNIPROT:P29676; GB:D10763; NID:g220735; PIDN:BA01593.1; PID:g220736
A;Cross-references: UNIPROT:P29676; GB:D10763; NID:g220735; PIDN:BA01593.1; PID:g220736
A;Cross-reference number: 146083; MUID:93372347; PMID:8364201
A;Accession: I62743
A;Accession: I62743
A;Accession: I62743
A;Accession: MRNA
A;Molecule type: mRNA
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A.Cross-references: GB:L10608; NID:g204060; PIDN:AAA41126.1; PID:g204061
C.Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c; Function:
A.Pescription: the primary inducer of erythrocyte formation
C.Superfamily: erythropoietin
C.Superfamily: erythropoietin
C.Superfamily: erythropoietin
F.1-26/Domain: signal sequence #status predicted <SIG>
F.27-192/Product: erythropoietin #status predicted <AMI>
F.33-187,55-165/Disulfide bonds: #status predicted
F.33-187,55-165/Disulfide bonds: #status predicted
F.50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: 146401; 147077
R;Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A;Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on pareference number: 146401; MUID:93351736; PMID:8349021
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                                                                     VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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82.5%; Pred. No. 2
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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Matches 137; Conservative
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ATP-dependent helicase HrpB [imported] - Salmonella enterica subsp. enterica serovar Typ
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Reference number: AB0502; MUID:21534947; PMID:11677608
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A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jun-2003
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A;Molecule type: DNA
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Cispecies: Isobility 1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
Cispecies: Isobility 1993
A.Title: Brythropoietin structure-function relationships: High degree of sequence homology, River commer: I46083; MUID:93372347; PMID:8364201
A.Recession: I46578
A.Recession: I46578
A.Recession: I46578
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-190 cWBN>
A.Residues: 1-190 cWBN>
A.Coss.references: UNIPROT:P49157; GB:L10607; NID:g164445; PIDN:AAA31029.1; PID:g164446
C;Superfamily: erythropoietin
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                                                                                                                                                                                                                                                                                                           69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                              27 APPRLICDSRVLERYILEAKEAENVTMGCAEGPRLSENITVADTKVNFYAWKRMEVEEQA 86
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                                                                                                                                                         9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTXVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 PPDTTPPAPLRTLTVDTFCKLFRVYANFLRGKLKLYTGEVCRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
Length 192;
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Query Match 76.7%; Score 686; DB 1; Best Local Similarity 79.5%; Pred. No. 1.8e-57; Matches 132; Conservative 14; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.7%;
Best Local Similarity 81.4%;
Matches 136; Conservative 1
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C.Genetics:
A.Gene: epo
C.Superfamily: erythropoietin
C.Keywords: glycoprotein; kidney
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erythropoietin - dog (fragment)
Cispecies: Canis lupus familiaris (dog)
Cjate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
CjAccession: 146199
R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 199
A;Title: Erythropoietin structure-function relationships: High degree of sequence homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;cross-references: UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
C;Superfamily: erythropoietin
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                                                                                                                                                   23 APPRLICDSRVLERYILBAKEGENATMGCAESCSFSENITVPDTKVNFYAWKRMEVQQQA
                                                                                                         9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                         129 PPDA---ASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGBACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
71.4%; Score 638; DB 2; Length 175;
Best Local Similarity 81.0%; Pred. No. 5.6e-53;
Matches 124; Conservative 13; Mismatches 16; Indels
  Length 190
                                                       21; Indels
Score 683; DB 2;
Pred. No. 3.4e-57;
7; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
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A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKL
     Query Match
Best Local Similarity 82.1%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-175 < WEN>
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A;Residues: 1-813 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01350.1; PID:g16501478; GSPDB:GN00176

C;Genetics: A;Gene: STY0214

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A;Accession: $48740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.353 < SOH)
A;Cossion: 1.354 < SOH)
A;Cossion: 1.354 < SOH)
B;Cossion: 1.354 < SOH
A;Cossion: 1.354 < SOH
A;Cossion: 1.355 < SOH
B;Cossion: 1.354 < SOH
B;Cossion: 1.355 < SOH
B;Cossion: 1.355 < SOH
B;Cossion: 1.355 < SOH
B;Cossion: 1.355 < SOH
B;Cossion: 1.38672
                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:L33410; NID:g506826; PIDN:AAA59857.1; PID:g506827
R;Sohma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
EBS Lett. 353, 57-61, 1994
A;Title: Molecular Cloning and Chromosomal localization of the human thrombopoietin gene
A;Reference number: S48740; MUID:95010765; PMID:7926023
                   A,Cross-references: GB:L36052; NID:g533216; PIDN:AAC37566.1; PID:g533217
R,de Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Yersinia pestis
C; Species: Yersinia pestis
C; Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: AB0323
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R; Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genomic structure, chromosomal localization, and conserved alternative splice A;Reference number: IS2610; MUID:95152076; PMID:7849319
                                            Ride Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, D.V.; Eaton, D.L.
Nature 369, 533-538, 1994
A;Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl ligand. A;Reference number: 845331; MUID:94261202; PMID:8202154
A;Recession: 845331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U11025; NID:9511223; PIDN:AAA50553.1; PID:9558078
R;Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
A;Title: Genomic structure, chromosomal localization, and conserved alternative splines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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A;Residues: 1-353 <RE4>
A;Cross-references: GB:S76771; NID:g914225; PIDN:AAB33390.1; PID:g914226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.0%; Score 89; DB 2; Length 353; 26.3%; Pred. No. 1.1;
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A,Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Reywords: alternative splicing; cytokine; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 -LPPQG------RTTAHKDPNAIFLSFQHLLRGKVR 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-112,'E',114-353 <RE3>
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Matches 41; Conserva
                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-353 <SAU>
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A;Accession: 180105
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-553 <RES>
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A;Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246
C;Genetics:
A;Gene: hTPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombopoietin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02729
R;Im, S.
                                                                                                                                                                                           1 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
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                                                                            Length 813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 90; DB 2; Length 353, 26.3%; Pred. No. 0.87;
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                                                               Query Match 10.2%; Score 91.5; DB 2; Best Local Similarity 27.1%; Pred. No. 1.7; Matches 45; Conservative 20; Mismatches 46;
C;Superfamily: ATP-dependent RNA helicase, HrpB type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
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A;Status: translated from GB/EMBL/DDBJ
Molecule type: DNA
A;Residues: 1-353 <RE2>
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Matches 41; Conserv
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A, Title: Genome sequence of Yersinia pestis, the causative agent of plague.

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C;Species: Salmonella enterica subsp. enterica servara Typhi
A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date. 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0959
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P.; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serva A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <PAR>A;Residues: 1-346 <PAR>A;Residues: 1-346 <PAR>A;Residues: T346 <PAR>A;Residues: SH3382; PIDN:CAD03169.1; PID:g16504804; GSPDB:GN00176
C;Genetics: A;Genetics: A;Gen
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB023
A;Status: preliminary
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8ZDC8; GB:AL590842; PIDN:CAC92889.1; PID:g15980631; GSPDB:GC;Genetics:
A;Gene: nrdF
C;Superfamily: ribonucleoside-diphosphate reductase beta
C;Keywords: oxidoreductase
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Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar
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9.8%; Score 88; DB 2; Length 323;
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Matches 34; Conservative 20; Mismatches 59; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 19, 2004, 20:59:03 ; Search time 103.996 Seconds (without alignments) 962.682 Million cell updates/sec Run on:

US-10-014-363-3 894 1 APPRIEGRAPPRLICDSRVL......NFLRGKLKLYTGEACRTGDR 174 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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### ALIGNMENTS

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POLISES: OBURZO: CITALIANS PRINCES: POLISES: POLISES: OBURZO:	BEDO HUMAN  BYANDARD;  POUS GOUEZS;  QUUHANG;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  10-OCT-2004 (Rel. 01, Last sequence update)  Brythropoietin precursor (Epoetin).  Name=EPO;  Homo sapiens (Human)  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TAXID=8606;  [1]  SEQUENCE FROM N.A.  MEDLINE=85137899; PubMed=3838366;  Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.  MUESON A., Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Myake T.;  "Isolation and characterization of genomic and cDNA clones of hu erythropoietin.";  "Isolation and characterization of genomic and cDNA clones of hu erythropoietin.";  REDUINE=86067948; PubMed=3865178;  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  MEDLINE=86067948; PubMed=3865178;  Cloning and expression of the human erythropoietin gene.";  Cloning and expression of the human erythropoietin gene.";  Cloning and expression of two human crythropoietin pene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).  SEQUENCE FROM N.A.  MEDLINE=90181818; PubMed=9799793;  Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,  Tsui LC., Rosenthal A.;  "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes.";  Genome Res. 8:1060-1073(1998).  RUBERT JL., Hochachka P.W.;  RUBERT JL., Hochachka P.W.;  RUBERT JL., Hochachka P.W.;  RUBERT JL., ROBHACHA P.W.;  RUBERT JL., Hochachka P.W.;  RUBERT JL., Hochachka P.W.;  RUBERT JL., Hochachka P.W.;  RUBERT JL., Hochachka P.W.;  RUBHA JL., Hochachka P.W.;
POISES: OBUEZO: OBUEZO	BEDO HUMAN  BYANDARD;  POUS GOUEZS;  QOUEZS;  Line septions  Real 45, Last annotation update)  Brythropoietin precursor (Broetin).  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  [1] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi  NCBL TAXID=8606;  [1] Acobs K.; Shoemaker C.; Rudersdorf R.; Neill S.D.; Kaufman R.J.  MEDLINE=85137899; PubMed=383856;  Jacobs K.; Shoemaker C.; Rudersdorf R.; Neill S.D.; Kaufman R.J.  MEDLINE=85137899; PubMed=383856;  Macbo A.; Shoemaker C.; Radersdorf R.; Fritsch B.F.;  Kawakita M.; Shimizu T.; Miyake T.;  "Isolation and characterization of genomic and cDNA clones of husure T. S. Suggs S.; Lin CH.; Browne J.K.; Smalling R.; Egrie  Erythropoietin.";  Nature 31:360-810(1985).  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  Lin R.K.; Suggs S.; Lin CH.; Browne J.K.; Smalling R.; Egrie  Chen K.K.; Pox G.M.; Martin F.; Stabinsky Z.; Badrawi S.M.; Lain R.C.; Nos G.M.; Martin F.; Stabinsky Z.; Badrawi S.M.; Lain Goldwasser E.;  "Cloning and expression of the human erythropoietin gene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).  [3]  SEQUENCE FROM N.A.  MEDLINE=9018118; PubMed=9799793;  Gloeckner G.; Scherer S.; Schattevoy R.; Boright A.P.; Weber J.;  "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes.";  Genome Res. 8:1060-1073(1998).  [4]  SEQUENCE FROM N.A.  Rupert J.L.; Hochachka P.W.;
POISES: QUEEZS; QUENAG; PARTITION POISES: DETAILMENT OF THE POISES: QUENCES; QUENCES	BEDGHUMAN STRANDARD; PRT; 193 AA. POUJ588; OSUDZO; GOUEZS; QUUHAQ; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human) Bidaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TAXID=5066; SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MAGEONA A. Seehra J. Jones S.S.; Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). SEQUENCE FROM N.A. MEDLINE=99018118; PubMed=9799793; Glockher G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes."; TSUI LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes."; Ruper T. S., Scherer S., Schattevoy R., Boright A.P., Weber J., TSUI LC., Rosenthal A.; "Large-scale scales of genomic sequence around the EPO and CUTLI reveals 17 genes."; Ruper T. J. Genes B. J.
POLSOBA: QUODZO; QUEEZS; QUUHAO; POLSOBA: QUODZO; QUEEZS; QUUHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last annotation update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 02-OCT-2004 (Rel. 02, Last sequence update) 03-OCT-2004 (Rel. 03) 04-OCD (Rel. 03) 04-OCD (Rel. 03) 04-OCD (Rel. 03) 04-OCD (Rel. 03) 05-OCT-2004 (	BEDO HUMAN  BYANDARD;  POUT 1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  12-UUL-1986 (Rel. 01, Last sequence update)  12-UUL-1986 (Rel. 01, Last sequence update)  Brythropoietin precursor (Bpoetin).  Name=ERO;  Homo sapiens (Human)  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TAXID=8606;  [1]  SEQUENCE FROM N.A.  MEDLINE=85137899; PubMed=3838366;  Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.  Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of huerythropoietin.";  [2]  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.;  "Cloning and expression of the human erythropoietin gene.";  Cloning and expression of the human erythropoietin pene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).  [3]  Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.;  "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUILI reveals 17 genes.";  Gloeckner FROM N.A.  MEDLINE-99018118; PubMed=9799793;  Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.;  "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUILI reveals 17 genomic 17 genomic 18 genomic sequence around the EPO and CUILI reveals 17 genomic 18 genomic 20 ge
POLSBB; Q9UDZO; Q9UEZO; Q9UBZO; Craated) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Rame=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] Ascobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Machina M., Shimizu T., Miyake T.; MEDLINE=8013899; PubMed=3838366; SEQUENCE FROM N.A. MEDLINE=80667948; PubMed=3865178; Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=80667948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] Glocckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Targe-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI Genome Res. 8:1060-1073(1998).	POLIGOR STANDARD;  PRT; 193 AA.  POLIGOR GRAINOR, STANDARD;  21-JUU-1986 (Rel. 01, Created)  21-JUU-1986 (Rel. 01, Last sequence update)  01-CCT-2004 (Rel. 01, Last sequence update)  01-CCT-2004 (Rel. 01, Last sequence update)  10-CCT-2004 (Rel. 01, Last sequence update)  10-CCT-2004 (Rel. 01, Last sequence update)  10-CCT-2004 (Rel. 01, Last annotation update)  10-CCT-2004 (Rel. 01, Last annotation update)  10-CCT-2004 (Rel. 01, Last annotation update)  10-CCT-2004 (Rel. 01, Last annotation)  10-CCT-2004 (Rel. 01, Released)  10-CCT-2004 (Rel. 01, Released)  10-CCT-2004 (Rel. 01, Released)  10-CCT-2004 (Rel. 01, Rel. 01, Rel
POLSBB; Q99UDZ0; Q9UEZ5; Q9UHA0; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Least sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=6813699; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mulson A., Seblira J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huse trythropoletin."; Nature 313:806-810(1985). [2] Nature 313:806-810(1985). [3] SEQUENCE FROM N.A. MEDLINE=6067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Coldwasser E.; "Cloning and expression of the human erythropoietin gene."; Cloning and expression of the human erythropoietin gene."; [3] Cloning and expression of two regions in human chromosome 7q22: MEDLINE=90108118; PubMed=9799793; Gloeckner G., Scherer S., Schartevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes."; [4] SEQUENCE FROM N.A.  "Large-scale Sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes."; SEQUENCE FROM N.A.	POLIGOR STANDARD; PRT; 193 AA.  POLIGOR GRAINOR STANDARD; POLIGOR GRAINOR, GOUEZS; QOUNDAG; 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Brythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDLINE=8137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDLINE=8137899; PubMed=385578; Isolation and characterization of genomic and cDNA clones of hu Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=80607948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE FROM N.A. MEDLINE=9018118; PubMed=9799793; Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes."; Genome Res. 8:1060-1073(1998). [4] SEQUENCE FROM N.A.
POLSBB; QUUDZO; QUEEZS; QUENAC; POLSBB; QUEDZO; QUEEZS; QUENAC; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last sequence around the EPO and Characterization of genomic and cDNA clones (I) 01-CCT-0205 K., Shommaker C., Rudersdorf R., Neill S.D., Kaufman R.J. 02cobs K., Shommaker C., Rudersdorf R., Neill S.D., Kaufman R.J. 03cobs K., Shommaker C., Rudersdorf R., Neill S.D., Kaufman R.J. 03cobs K., Shommaker C., Rudersdorf R., Neill S.D., Kaufman R.J. 03cobs K., Shommaker C., Edspinsky Z., Badrawi S.M., Lai SEQUENCE FROM N.A. 03. MEDLINE-86067494 PubMed=3865178; 03. Maction and expression of the human erythropoietin gene."; 03. Cloning and expression of the human erythropoietin gene."; 03. Cloning and expression of the human erythropoietin gene."; 04. Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). 05. SEQUENCE FROM N.A. 06. MEDLINE-99018118; PubMed=9799793; 06. MEDLINE-99018118; PubMed=9799793; 07. Tsui LC., Rosenthal A.; 07. Tsui L	POLSOBS, OSUBORND, PRT; 193 AA. POLSOBS, OSUBORO, OSUBORO
POLSBB; Q9UDZO; Q9UEZO; Q9UHAO; POLSBB; Q9UDZO; Q9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; 21-UUL-1986 (Rel. 01, Created) 01-OCT-2004 (Rel. 45, Last sequence update) 01-OCT-2004 (Rel. 45, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Homo sapiens (Human)  Expthropoietin precursor (Epoetin). NGH TaxID=9606;  L1] SEQUENCE FROM N.A. MEDLINE=80137899; PubMed=3838366; SEQUENCE PROM N.A. MEDLINE=80137899; PubMed=3838366; SEQUENCE PROM N.A. MEDLINE=801041 T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86667448; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lain FK., Suggs S., Lin CH., Browne J.K., Sadrawi S.M., Lain FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lain FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lain FK., Sox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lain FK., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lain LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI Genome Res. 8:1060-1073(1998).	PUTE-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 01, Last sequence update) Name=EPO; Homo sapiens (Human) NGME-EPO; Homo sapiens (Human) NGME-EPO; Homo sapiens (Human) NGMI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=88131899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MUEON A., Sehera J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of hu ufson A., Sabara V., Sandara V., Sandara V., Jones S.S., Hewick R., Fritsch B.F., Naufson A., Sabara V., Jones S.S., Hewick R., Fritsch B.F., "Isolation and characterization of genomic and cDNA clones of hu erythropoietin.", Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] Glockner G., Scherer S., Schattevoy R., Boright A.P., Weber J., "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI Genome Res. 8:1060-1073(1998).
POLSBB; Q9UDZO; Q9UEZO; Q9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last annotation update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last annotation update) 01-OCT-2004 (Rel. 02, Last C., Rudersdorf R., Neill S.D., Kaufman R.J. 01-OCT-2005 K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. 01-OCDENCE PROM N.A. 01-OCT-2004 (Rel. 02, Lanc CH., Browne J.K., Smalling R., Egrie erythropoletin.") 02-OCT-2004 (Rel. 02, Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; 03-OCT-2004 (1985) 03-OCT-2004 (1985) 04-OCT-2004 (1985) 05-OCT-2004	EPO HUMAN STANDARD; PRT; 193 AA. P01588; O9UEZO; Q9UEZO; Q9UEZO; Q9UEZO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Brythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDLINE=8137899; PubMed=385578; Jacobs M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of hu Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE FROM N.A. MEDLINE=9018118; PubMed=9799793; Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes.";
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POLSBB; QUUDZO; QUEEZ; QUUHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence Carrible (Rel. 02, Last sequence Rel. 03, Last sequence Carrible (Rel. 03, Last sequence Carrible (Last sequence Carrible (Carrible (Last sequence Carrible (Carrible (Carrible (Last sequence Carrible (Carrible (Ca	PUTENDY STANDARD; PRT; 193 AA. PUTE-1986 (Rel. OL, Created) 21-JUL-1986 (Rel. OL, Created) 21-JUL-1986 (Rel. OL, Created) 21-JUL-1986 (Rel. OL, Created) 21-JUL-1986 (Rel. OL, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Homo sapiens (Human) NGME-EPO; Homo sapiens (Human) NGME-EPO; Homo sapiens (Human) NGBI TaxID=9606; [1] SEQUENCE PROM N.A. MEDLINE=88133839; PubMed=3838366; MACODS K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MACOLALIA M., Shimizu T., Miyake T.; Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huserythropoietin."; "Isolation and characterization of genomic and cDNA clones of huserythropoietin."; "SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE FROM N.A. MEDLINE=99018118; PubMed=9799793; Glocckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI Prevener R. Parker R. Pa
POLSBB; Q9UDZO; Q9UEZO; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=8013099; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mulson A., Seblira J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] Nature 313:806-810(1985). [3] SEQUENCE FROM N.A. MEDLINE=8067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Cloning and expression of the human erythropoietin gene."; [3] REQUENCE FROM N.A. MEDLINE=9010118; PubMed=9799793; Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI reveals 17 genes.";	PEPO HUMAN  STANDARD;  PO1588; O9UEZO;  209UHAGO;  21-JUJ-1986 (Rel. 01, Created)  21-JUJ-1986 (Rel. 01, Last sequence update)  01-OCT-2004 (Rel. 45, Last annotation update)  101-OCT-2004 (Rel. 45, Last annotation update)  102-CT-2004 (Rel. 45, Last annotation update)  103-CM-2004 (Rel. 45, Last annotation update)  104-CM-2004 (Rel. 45, Last annotation update)  105-CM-2004 (Rel. 45, Last annotation update)  106-CM-2005 K., Shomeraer C., Rudersdorf R., Neill S.D., Kaufman R.J., Mulson A., Sehlma C., Jones S.S., Hewick R., Fritsch B.F.,  107-CM-2005 K., Shimizu T., Miyake T.;  108-CM-2006 M., Martin F., Stabinsky Z., Badrawi S.M., Laiden K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Laidelle R. C., Martin F., Stabinsky Z., Badrawi S.M., Laidelle R. C., Martin R., Scherer S., Schartevoy R., Boright A.P., Weber J., SEQUENCE FROM N.A.  131-CL, Rosenthal A.;  132-CLOINING SCHORE RROM N.A.  133-CLOINING Scherer S., Schartevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.;  134-CR-2018 M. M. Martin R. Schartevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.;  135-CR-2018 M.
POLSER: QUEDZO: CARREAGO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last sequence update) 01-CCT-2004 (Rel. 45, Last sequence update) Name=BO; Name=BO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDILNE=86137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDILNE=86137899; PubMed=385178; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDILNE=86137899; PubMed=385178; Isolation and characterization of genomic and cDNA clones of huserythropoietin "; SEQUENCE FROM N.A. MEDILNE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). SEQUENCE FROM N.A. MEDILNE=99018118; PubMed=9799793; Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI	POLIGOR DEPO HUMAN STANDARD; PRT; 193 AA. POLIGOR (PRE). 03 CREATE, 209UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) Erythropotetin precursor (Epoetin). Name=EPO; Homo sapiens (Human) NCBI Tax1D=9606; Homo sapiens (Human) NCBI Tax1D=9606; [1] SEQUENCE PROM N.A. MEDLINE=86137899; PubMed=3838366; Machia H. Shimizu T., Miyake T.; Machia M., Shimizu T., Miyake T.; Rawakita M., Shimizu T., Miyake T.; Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE PROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK.; Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; "Tsui LC., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7022: "Large-scale sequencing of two regions in human chromosome analysis of 650 kb of genomic sequence around the EPO and CUTLI
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POLSOBAL GOUDZO, SOLANDERS, GOUDRA, POLSOBAL, DEPOLSOBAL SOLANDERS, GOUDZO, SOLANDERS, GOUDRA, SOLANDERS, GOUDRA, SOLATOL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 04, Last sequence update) 01-OCT-2004 (Rel. 04, Last sequence update) 01-OCT-2004 (Rel. 04, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=10	PO1588; Q9UDGO; Q9USEAS; Q9UHAQO; 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoletin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE PROM N.A. MEDLINE=86137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Muteon A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; Fewick R., Fritsch B.F., "Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE PROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE PROM N.A. MEDLINE=9018118; PubMed=9799793; Gloeckner G., Scherter S., Schattevoy R., Boright A.P., Weber J., Tsui LC., Rosenthal A.;
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POLSES: QUECA: CANDEANO, STANDARD, 193 MA.  POLSES: QUECA: CASTES: QUECA: LAST SEGUENCE UPDATE: L93 MA.  21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 02, Last sequence update) 01-OCT-2004 (Rel. 04). Last sequence update) Brythropoletin precursor (Epoetin). Name=EPO: Name=EPO: Name=EPO: Name=EPO: Name=10: Primates: Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates: Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE PROM N.A. MEDLINE=8013899; PubMed=3838366; MACTOR K. Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mufson A., Shehra J., Jones S.S., Hewick R., Fritsch E.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE PROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE PROM N.A. MEDLINE=90018118; PubMed=9799793; Gloeckner G., Scherer S., Schaffevov R., Roricht A. D. Waher J. Gloeckner G., Scherer S., Schaffevov R., Medline J. D., Medline J. J. D., Medline J. J. Scherer S., Schaffevov R., Medline J. D., Medline J. J. J. Scherer S., Schaffevov R., Medline J.	POLIGNAN  EPO HUMAN  STANDARD;  POLIGNAN  POLIGNAN  POLIGNAN  21-JUL-1986 (Rel. OL, Created)  21-JUL-1986 (Rel. OL, Created)  21-JUL-1986 (Rel. OL, Last sequence update)  OL-OCT-2004 (Rel. 45, Last annotation update)  Erythropoletin precursor (Epoetin).  Name=EPO;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TaxID=9606;  [1]  SEQUENCE FROM N.A.  MEDLINE=6137899; PubMed=3838366;  Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.  Mutson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of hu  erythropoletin.";  Nature 313:806-810(1985).  [2]  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie  Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai  Goldwasser E.;  "Cloning and expression of the human erythropoietin gene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).  [3]  SEQUENCE FROM N.A.  MEDLINE=90018118; PubMed=9799793;  Gloeckner G., Scherer S., Schaffevov R., Roricht A. D. Waher J.  MEDLINE=90018118; PubMed=9799793;  Gloeckner G., Scherer S., Schaffevov R., Roricht A. D. Waher J.  MEDLINE=90018181 PubMed=9799793;
POLSEB: OPPOZO: OPPOZO: OPPOZO: POLSE: 193 MA. POLSEB: OPPOZO:	POLIGOR DEPO HUMAN STANDARD; PRT; 193 AA. POLIGOR (PUNAN STANDARD; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Brythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. MEDLINE=86137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., Mufson A., Shehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huserythropoietin."; "Isolation and characterization of genomic and cDNA clones of huserythropoietin."; "Isolation and characterization of genomic and cDNA clones of huselline ReNG Pages PubMed=3865178; "Isolation and characterization of the human erythropoietin gene."; Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).  SEQUENCE FROM N.A. MEDLINE=99018118; PubMed=9799793;
POLSEB: OPUZORO, SOUTHAND. POLSEB: OPUZORO, SOUTHAND: 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last amnotation update) Erythropoietin precursor (Epoetin). Brythropoietin precursor (Epoetin). Homo sapiens (Human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=86137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., Kawakita M., Shimizu T., Miyake T.; Misolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE FROM N.A. MEDLINE=9018118. PubMed=9799793.	POLIGOR DEPO HUMAN STANDARD; PRT; 193 AA. POLIGOR GREL OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Last sequence update) 01-OCT-2004 (Rel. OI, Last sequence update) 01-OCT-2004 (Rel. OI, Last sequence update) Erythropoletin precursor (Epoetin). Name=EPO; Homo sapiens (Human) NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=89139899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mufson A., Sehera d., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; "Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; "SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Sugges S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985). [3] SEQUENCE FROM N.A. MEDLINE=9018118. PubMed=979973.
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POLSB8; OBDZO, QUECES; QUHANO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 04, Last sequence update) 01-OCT-2004 (Rel. 04). Last sequence update) Erythropoietin precursor (Epoetin). Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE PROM N.A. MEDLINE=8131989; PubMed=3838366; Jacobs K., Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Maclion A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Nawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).	PEPO HUMAN  STANDARD;  PRT; 193 AA.  PO1568; O9UHZAS; O9UHAQO;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  01-OCT-2004 (Rel. 45, Last annotation update)  Brythropoietin precursor (Epoetin).  Name=EPO;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TaxID=9606;  [1]  SEQUENCE FROM N.A.  MADDILINE=86131889; PubMed=3838366;  Jacobs K.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.  Mufson A.; Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Rawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of hu erythropoietin.";  Nature 313:806-810(1985).  [2]  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  MEDLINE MEDLI
POLSES, OSUDZO, STANDANCE, COURAGE 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 04), Last sequence update) 01-CCT-2004 (Rel. 04), Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; NGBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDILNE=ES137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDILNE=ES137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDILNE=ES137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDILNE=ES137899; PubMed=3865178; Isolation and characterization of genomic and cDNA clones of humare 313:806-810(1985). [2] Nature 313:806-810(1985). Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Islace. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).	PEPO HUMAN  PEPO HUMAN  PARANDARD;  PO1589;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  01-0CT-2004 (Rel. 45, Last annotation update)  01-OCT-2004 (Rel. 45, Last annotation update)  Erythropictin precursor (Epoctin).  Name=EPO;  Name=EPO;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TaxID=9606;  [1]  SEQUENCE FROM N.A.  MEDLINE=85137899; PubMed=3838366;  Jacobs K., Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J.  Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of hu erythropoietin.";  Nature 313:806-810(1985).  [2]  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.;  "Cloning and expression of the human erythropoietin gene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1985).
POLSB8; OSUDZO; OSUBZES; OSUBANO; 21-JUL-1986 (Rel. 01; Created) 21-JUL-1986 (Rel. 01; Created) 21-JUL-1986 (Rel. 01; Created) 21-JUL-1986 (Rel. 01; Last sequence update) 01-CCT-2004 (Rel. 05; Last annotation update) 01-CCT-2004 (Rel. 45; Last annotation update) Erythropoietin precursor (Epoetin). Name=EDO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9666; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of humbline=86067948; PubMed=3865178; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584 (1995).	BEDO HUMAN  STANDARD;  PO1588; O9UDZO; Q9UEZS; O9UHAO;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  21-UUL-1986 (Rel. 01, Last sequence update)  21-UUL-1986 (Rel. 01, Last sequence update)  10-CCT-2004 (Rel. 45, Last annotation update)  Brythropoietin precursor (Epoetin).  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TAXID=9606;  [1]  SEQUENCE FROM N.A.  MEDLINE=85137899; PubMed=3838366;  Jacobs K., Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., MacEDLINE=85137899; PubMed=3838366;  Jacobs K., Sheemaker C., Mayake T.;  "Isolation and characterization of genomic and cDNA clones of huserythropoietin.";  "Isolation and characterization of genomic and CDNA clones of huserythropoietin.";  Nature 313:806-810(1985).  [2]  SEQUENCE FROM N.A.  MEDLINE=86067948; PubMed=3865178;  Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai C.Choning and expression of the human erythropoietin gene.";  Proc. Natl. Acad. Sci. U.S.A. 82:7580-7584(1995).
POLSB8; ONDEOS, QUENTES; QUHANG; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 04, Last sequence update) Erythropoietin precursor (Epoetin). Enwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE PROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., MacDaltion and Characterization of genomic and cDNA clones of huerythropoietin.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai "Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad Sci. 11 S. A. R., Sradias,	PEPO HUMAN STANDARD; PRT; 193 AA. P01588; O9UEZO; Q9UEZO; Q9UEZO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxDE=9606; [1] SEQUENCE FROM N.A. MEDILINE=86137889; PubMed=3838366; Jacobs K.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Muffon A.; Schemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Muffon A.; Schemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Muffon A.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Muffon A.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mufson A.; Schema V., Jones S.S., Hewick R., Fritsch B.F., "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin RK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; Cloning and expression of the human erythropoietin gene."; Proc. Natl. Acad Sci. 11 S. A. 20.75RA(1928)
POLISBB: ONDEOS, ONDEOS; ONDEO	PEPO HUMAN STANDARD; PRT; 193 AA. P01588; O9UEZO; Q9UEZO; Q9UEZO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) 01-0CT-2004 (Rel. 45, Last annotation update) Erythropictin precursor (Epoctin). Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Tsolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai Goldwasser E.; "Cloning and expression of the human erythropoietin gene.";
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POLSES: OSUDZO; QSUEZS; QSUHAN; POLSES: OSUDZO; QSUEZS; QSUHAN; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last sequence update) 01-CCT-2004 (Rel. 45, Last sequence update) Name=Epo; Name=Epo; Name=Epo; Name=Epo; Nome=Epo;	BEDO HUMAN STANDARD; PO1588; O9UDZO; Q9UEZS; O9UHAQO; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. O1, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). BUKARYOta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=86137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of hu erythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin FK., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie Chen K.K., Fox G.M., Martin F., Stabinsky Z., Badrawi S.M., Lai
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POLISES, OSUDZO, STANDAND, 21-012, 193 AA.  POLISES, OSUDZO, QUUEZS, QUUHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 05, Last sequence update) 01-CCT-2004 (Rel. 05, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=Ini Butheria; Primates; Craniata; Vertebrata; Buteleostomi Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo. NCBI TaxD=9606; [1] SEQUENCE PROM N.A. MEDLINE=68137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. Mufson A., Sehra J., Jones S.S., Hewick R., Fritsch E.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; Nature 313:806-810(1985). [2] SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin F.K., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie	PEPO HUMAN STANDARD; PRT; 193 AA. PO1589; O9UDZO; Q9UEZS; Q9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 01, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; NCBI_TAXID=9606; [1] SULARIDE PROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K.; Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MEDLINE=85137899; PubMed=3838366; Jacobs K.; Sheemaker C., Rudersdorf R., Neill S.D., Kaufman R.J. MISOLATION and characterization of genomic and cDNA clones of huerythropoietin."; "Isolation and characterization of genomic and cDNA clones of huerythropoietin."; SEQUENCE FROM N.A. MEDLINE=86067948; PubMed=3865178; Lin F. K., Suggs S., Lin CH., Browne J.K., Smalling R., Egrie
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PUISBS, QUUDZO, CORRESS, QUURAD, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Name-EPO; Name-EPO; Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxLD-9666; [1] SEQUENCE FROM N.A. MEDLINE-85137899; PubMed=3838366; Macfoobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Warstia M., Shimitu T., Miyake T.; Isolation and characterization of genomic and cDNA clones of erythropoietin."; Rolation and sharacterization of genomic and cDNA clones of Nature 313:806-810(1985). SEQUENCE FROM N.A. MEDLINE-866067948; PubMed=3865178; MEDLINE-86067948; PubMed=3865178;	BEO HUMAN  BEO HUMAN  STANDARD;  PO1588, O9UDZO;  SUGUEZS; O9UHAO;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  01-OCT-2004 (Rel. 45, Last annotation update)  Erythropoietin precursor (Epoetin).  Name=EPO;  Name=EPO;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc  Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.  NCBI TaxID=966;  [1]  SEQUENCE FROM N.A.  MEDDINE=85137899; PubMed=3838366;  Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.  Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,  Rawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of erythropoietin.";  Nature 313:806-810(1985).  SEQUENCE FROM N.A.  MEDLINE=66067948; PubMed=3865178;
POLISES, OSUBZO, OSUBEZS, OSUBAD.  21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 01, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; NGBI TaxID=966; 101 TaxID=966; 113 TaxID=966; 125 SEQUENCE PROM N.A. MEDLINE=65137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R. Mufsbilns=65137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R. Mufsbilns=1010 and characterization of genomic and cDNA clones of erythropoletin; 180lation and characterization of genomic and cDNA clones of erythropoletin; 1818CHENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A.	POUT HUMAN  POUD STANDARD;  POUT BB8;  POUD STANDARD;  POUT BB8;  POUD STANDARD;  POUT BB8;  POUD STANDARD;  POUT BB8;  P
POLSES, OSUBZO, OSUBZOS, OSUBZO, OSUBZOS, OSUBZO	BEOLHUMAN STANDARD; PRT; 193 AA. P01589; OGUDZO; QGUEZS; OGUHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name-EPO; Homo sapiens (Human) Name-EPO; Homo sapiens (Human) NEULINESEROR Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=89137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Makkita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; "Nature 313:806-810(1985). [2] SEQUENCE FROM N.A.
POISBS: OSUBZO: OSUBZOES,	BEO HUMAN  BY ANDRED; QUEZS; QUHAQ;  21-JUL-1986 (Rel. 01, Created)  21-JUL-1986 (Rel. 01, Created)  21-JUL-1986 (Rel. 01, Last sequence update)  21-JUL-1986 (Rel. 01, Last sequence update)  21-JUL-1986 (Rel. 01, Last sequence update)  BYCHACOPOIGTIN PRECURSOR (Epoetin).  Name=EPO;  Home sapiens (Human).  BUKARYOLS; Metazoa; Chordata; Craniata; Vertebrata; Buteleost Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  NCBI TaxID=9666;  [1]  SEQUENCE FROM N.A.  MEDIINE=681389366;  Jacobs K.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Sehma J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of erythropoietin.";  Nature 313:806-810(1985).  SEQUENCE FROM N.A.
PUISBS; QUUDZO; QUERZA; QUURAD; 21-JUL-1986 [Rel. 01, Created) 21-JUL-1986 [Rel. 01, Created) 21-JUL-1986 [Rel. 01, Last sequence update) 01-CCT-2004 [Rel. 01, Last sequence update) 01-CCT-2004 [Rel. 01, Last sequence update) Name=EPO; None sapiens (Human). Name=EPO; Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9664; [1] SEQUENCE FROM N.A. MEDLINE=86137889; PubMed=3838366; R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimitu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Nature 313:806-810 [1985).	BEOULHUMAN STANDARD; PRT; 193 AA. P01589, O9UDZ0; Q9UEZ5; O9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Name=EPO; NAME Sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MEDLINE=85137899; PubMed=3838366; MEDLINE=8013899; PubMed=3838366; Macfeon A., Seehra U., Jones S.S., Hewick R., Fritsch E.F., Mufeon A., Shemizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Commence 31:806-810(1985).
POLSES OURDED, COURTER, OBUTANO, PARISHED BY COURTED BY	BEO HUMAN STANDARD; POT SEQ HUMAN STANDARD; POT SEQ HUMAN STANDARD; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last amnotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human) Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Nature 313:806-810(1985).
POLISES, OSUBZO, OSUBEZA, OSUBADO, POLISES, DANDORO, OSUBEZA, OSUBADO, OSUBEZA, OSUBADO, OSUBEZA, OSUBADO, OSUBEZA, OSUBADO, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostt Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo. NCBI TaxID=5665, [1] SEQUENCE FROM N.A. MEDLINE=83137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Makkita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Nature 313:806-810(1985).	BEO HUMAN  BEO HUMAN  BEO HUMAN  PO1589, O9UDZO; Q9UEZS; O9UHAO;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  01-OCT-2004 (Rel. 45, Last amnotation update)  ETYCHOODIGIN precursor (Epoetin).  Name=EPO;  Homo capiens (Human)  Name=EPO;  Homo sapiens (Human)  NEBITAXID=8618;  Frimates; Catarrhini; Hominidae; Homo.  NEBITAXID=8619;  [1]  SEQUENCE FROM N.A.  MEDINE=88137899; PubMed=3838366;  Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of erythropoietin."  Nature 313:806-810(1985).
POLISES, OSUDEO, OSUGUEZA, OSUGRA, DELL'193 FAT.  21-JUL-1986 [Rel. 01, Created) 21-JUL-1986 [Rel. 01, Last sequence update) 21-JUL-1986 [Rel. 01, Last sequence update) 01-OCT-2004 [Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDILINE=6813893; PubMed=3838366; Jacobs K.; Shoemaker C.; Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Sehra J., Jones S.S., Hewick R., Fritsch E.F., "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Nature 313:806-810(1985).	BEO HUMAN  BY STANDARD;  POLTS BY OBUDZO;  POURZO;  POURALYOLA;  PO
PULDER, ONDERO, ONDERES, ONDERE, ONDERE, ONDERE, ONDERE, ONDERE, ONDERE, ONDERE, ONDERE, ONDE	BEO HUMAN STANDARD; PRT; 193 AA. P01588; O9UDZ0; Q9UEZ5; O9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Name=EPO; NAMEAZOA; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo. NCBI_TAXID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MEDLINE=85137899; PubMed=3838366; Muffson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F., Kawakita M., Shimiau T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin."; Nature 313:866-810.
POLSES OURDED, COURTER, OBUTA, DATE OF THE POLSES OUR OF THE POLSES OUR OLD OLD OUR OUR OLD OUR OUR OLD OUR OUR OLD OUR OUR OUR OUR OUR OLD OUR	BEO HUMAN STANDARD; PRT; 193 AA. PO1589; O9UDZO; Q9UEZS; O9UHAO; 21-UUL-1986 [Rel. 01, Created) 21-UUL-1986 [Rel. 01, Created) 21-UUL-1986 [Rel. 01, Last sequence update) 01-OCT-2004 [Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Home sapiens (Human) NAME=EPO; Home sapiens (Human) NCBI TaxID=9606; HOME TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=83137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Markita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin.";  NCKLE C. S.
POLISES, OSUBZO, OSUBZOS, OSUB	BEO HUMAN STANDARD; PRT; 193 AA. P01589; O9UDZ0; Q9UEZ5; O9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) ETYTHOODIGTIN precursor (Epoetin). Name=EPO; HOMO sapiens (Human). Name=EPO; HOMO sapiens (Human). NGEI TAXID=9606; [1] SEQUENCE FROM N.A. MEDINTE=681389366; JACODS K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropoietin.";
POLISES, OSUBZO, OSUBZA, OSUBAR, PARIS, 193 AM. POLISES, OSUBZO, OSUBZA, OSUBAR, PARIS, 193 AM. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last monotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDINTE=88137899; PubMed=3838366; Jacobs K.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F., Rawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of erythropojetin.";	BEO HUMAN  BEO HUMAN  POIDSB; OSUBZS; OSUBAO;  21-JUL-1986 (Rel. 01, Created)  21-JUL-1986 (Rel. 01, Created)  21-JUL-1986 (Rel. 01, Last sequence update)  01-OCT-2004 (Rel. 45, Last annotation update)  Erythropoietin precursor (Epoetin).  Name=EPO;  Name=EPO;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc  Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo.  NCBI TaxID=9606;  [1]  SEQUENCE PROM N.A.  MEDDINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R.  Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F.,  Kawakita M., Shimizu T., Miyake T.;  "Isolation and characterization of genomic and cDNA clones of erythropojetin.";
PUISBS, QUUDZO, CORREAS, QUURAD, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2094 (Rel. 01, Last sequence update) 01-CCT-2094 (Rel. 01, Last sequence update) Name=EPO; Name=EPO; Name=EPO; Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9666; SEQUENCE FROM N.A. MEDLINE=86137889; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdooff R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch B.F., Kawakita M., Shimitu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of	PUT-1996 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; NAME and CHUMAN). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MAEDLINE=85137899; PubMed=3838366; Muffson A., Shhemaker C., Rudersdorf R., Neill S.D., Kaufman R., Muffson A., Seehra J., Jones S.S., Kawakita M., Shimizu T., Miyake T.; "Isolation and characterization of genomic and cDNA clones of
POLSES OURDEO, CONTRICAND, PARTY, 193 AM. POLSES, COURDED, COURDES, COURDES, COURDES, 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) NAMM=EPO, NAMM=EPO, Human). Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9066; [1] TAXID=9066; [1] TAXID=9066; MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R. Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F., Kawakita M., Shinzu T., Miyake T.; Kawakita M., Schlar J., Taxidation and characterization of genowic and cDNA clones of	BPD HUMAN  BY STANDARD; PRT; 193 AA.  POISES; QUUDZO;
POLISES, OSUDZO, OSUGRES, OSUGRA, PARIS, 193 AM. POLISES, OSUGRES, OSUGRES, OSUGRA, OSUGRES, OSUGRE, O	BEO HUMAN STANDARD; POTEZS; OSUHAO; POTEZS; OSUHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Homo sapiens (Human). Name=EPO; Homo sapiens (Human). NEBLARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=89137899; PubMed=3838366; Aacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Markita M., Shimizu T., Miyake T.; "Isolation and characterization of Genomic and churcher of
POLSES: OBUDZO, OSUGUEZA, OBUHAO, 21-7UL-1986 (Rel. 01, Created) 21-7UL-1986 (Rel. 01, Created) 21-7UL-1986 (Rel. 01, Last sequence update) 21-7UL-1986 (Rel. 01, Last sequence update) 01-0CT-2004 (Rel. 01, Last sequence update) Brythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxII=9606; [1] SEQUENCE FROM N.A. MEDLINE=68137899; PubMed=3838366; Jacobs K.; Shoemaker C., Rudersdorf R., Neill S.D., Kaufman R., Mufson A., Seehra J., Jones S.S., Hewick R., Fritsch E.F., Rayakita M., Shimizu T., Miyake T.;	BEO HUMAN STANDARD; PRT; 193 AA. P01589; O9UDZ0; Q9UEZ5; O9UHAO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=BO; Name=B
DISBA: OBUDZO, OSTANARO, PERI, 193 AH.  DISBA: OBUDZO, OSTANARO, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last amotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, NCBI TaxID=9606, [I] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MAGEON A., Sebemaker C., Rudersdorf R., Neill S.D., Muffeon A., Seehra J., Jones S.S., Hewick R., Fritsch Kawakita M., Shimizu T., Miyake T.;	EPO HUMAN STANDARD; PRT; 193 AA. POIJS8; OGUDZO; QUEEZS; OGUHAO; 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Created) 21-JUL-1986 (Rel. OI, Last sequence update) 21-JUL-1986 (Rel. OI, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Homo sapiens (Human). Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TAXID=9606; [SI] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Muffson A., Seehra J., Jones S.S., Hewick R., Fritsch Kawakita M., Shimizu T., Miyake T.;
PULSES, OSUDZO, OSUGRAN, OSUGRA, PALIF, 193 AM.  21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Name=EPO; Nammalia; Eutheria; Primates; Catarrhini; Hominidae, NCBI TaxID=9666, [1] ASDUENCE PROM N.A. MEDLINE=5613/7899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Mukfson A., Seehra J., Jones S.S., Hewick R., Fritsch Kawakita M., Shimizu T., Mivake T.;	EPO HUMAN STANDARD; PD1589, Q9UDZO; Q9UEZS; Q9UHAO; P01589, Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammanlais Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Mufson A., Shoemaker C., Hewick R., Fritsch Kawakita M., Shimizu T., Mivake T.;
DECOURSE: OSTANDARD, PARIF, 193 AM. DECOURSE: OSTANDARDARD, PARIF, 193 AM. DECOURSE: OSTANDARDARD, PARIF, 193 AM. DECOURSE: OSTANDARDARD, PARIF, PARIF, PARIF, HOMINIDAE, NGMMANALIA; EULHERIA; PRIMATES; CATATRINII; HOMINIDAE; NGMMANALIA; EULHERIA; PRIMATES; CATATRINII; HOMINIDAE; 101 DECOURSE: OSTANDARDARDARD, PADMED-3838366; JACODS K., Shoemaker C., Rudersdorf R., Neill S.D., Mufson A., Soemaker C., Jones S.S., Hewick R., Fritsch Manalia, E., Company, Jacobs R., Shoemaker C., Jones S.S., Hewick R., Fritsch Manalia, M. Ostandard, Jacobs S.S., Hewick R., Fritsch	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEAS; O9UHAO; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, created) 21-UUL-1986 (Rel. O1, isst sequence update) 21-UUL-1986 (Rel. O1, isst sequence update) 21-UUL-1986 (Rel. O1, isst sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; NCBL TaxID=960; Il SEQUENCE PROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Muffeon A., Shoemaker C., Jones S.S., Hewick R., Fritsch Manalis A., Shoemaker S.S., Hewick R., Fritsch
DIOSES, OSUBLO, OSUBLO, OSUBLO, OSUBLO, OSUBLO, OSUBLO, OSUBLO, OSUBLO, OSUBLO, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last annotation update) 21-JUL-1986 (Rel. 01, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; Name=EPO; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=8013899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D., Muffson A., Seehra J., Jones S.S., Hewick R., Fritsch	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) ETYLAROPOICTIN PRECURSOR (Epoctin). Name=EPO; Name=EPO; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NGEI TAXID=9606; [1] SEQUENCE FROM N.A. MEDLINE=68138936; MAGCOBS K., Shoemaker C., Rudersdorf R., Neill S.D., Muffeon A., Seehra J., Jones S.S., Hewick R., Fritsch
DISBAN ONDERORY OF THE PRITT IN THE PRITT OF	EPO HUMAN STANDARD; PRT; 193 AA. P01589; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Homo sapiens (Human). Horinates; Catarrhini; Hominidae, NGEI TaxID=966; [1] SEQUENCE PROM N.A. MEDLINE-85137899; PubMed=3838366; MEDLINE-85137899; Aboemaker C., Rudersdorf R., Neill S.D., Mifson A., Seehra J., Jones S.S., Hewick R., Fritsch
DISBA: OBUDZO; OSTANDARO; PERI; 193 AH. DISBA: OBUDZO; OSTANDARO; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) Brythropietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MEDLINE=85137899; PubMed=3838366; Mufforn A. Sehemaker C., Rudersdorf R., Neill S.D., Jacobs K., Sehemaker C., Rudersdorf R., Neill S.D., Junes R., Sehemaker C., Rudersdorf R., Neill S.D., Junes R., Sehemaker C., Rudersdorf R., Pericoh	EPO HUMAN STANDARD; PRT; 193 AA. 20-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) 8-UCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Homo sapiens (Human). Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TAXID=9606; [SI] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; MEDLINE=85137899; PubMed=3838366; Mufforn A. Sehemaker C., Rudersdorf R., Neill S.D., Mufforn A. Sehemaker C., Rudersdorf R., Neill S.D., Mufforn A. Sehemaker C., Rudersdorf R., Pericoh
PUISBS: OBUDZO; OSTRUANDO, PARIT, 193 AH.  PUISBS: OBUDZO; OSTRESS; OBUHAO;  21-UUL-1986 (Rel. 01, Created)  21-UUL-1986 (Rel. 01, Last sequence update)  22-UUL-1986 (Rel. 01, Last sequence update)  23-UCCCT Sequence (Rel. 01, Last sequence update)  23-UCCT Sequence (Rel. 01, Last sequence update)  23-UCCT Sequence (Rel. 01, Last sequence update)  24-UUL-1986 (Rel. 01, Last sequence update)  24-UUL-1986 (Rel. 01, Last sequence update)  25-UUL-1986 (Rel. 01, Last sequence update)  25-UUL-1986 (Rel. 01, Last sequence update)  26-UUL-1986 (Rel. 01, Last sequence update)  27-UUL-1986 (Rel. 01, Last sequence update)  27-UUL-1986 (Rel. 01, Last sequence update)  28-UUL-1986 (Rel. 01, Last sequence update)  28-UUL-1986 (Rel. 01, Last sequence update)  28-UUL-1986 (Rel. 01, Last sequence update)  29-UUL-1986 (Rel. 01, Last sequence update)  29-UUL-1986 (Rel. 01, Last sequence update)  20-UUL-1986 (Rel. 01, Last sequence update)  20-UUL-1986 (Rel. 01, Last sequence update)  29-UUL-1986 (Rel. 01, Last sequ	BPO HUMAN STANDARD;  PRT; 193 AA.  POUD 890 BEO GRANDARD;  POUD 891 GOUD 1, Created)  21-JUL-1986 (Rel. 01, Created)  21-JUL-1986 (Rel. 01, Last sequence update)  21-JUL-1986 (Rel. 01, Last sequence update)  21-JUL-1986 (Rel. 01, Last sequence update)  81-JUL-1986 (Rel. 01, Last sequence update)  821-JUL-1986 (Rel. 01, Last sequence update)  821-JUL-1986 (Rel. 01, Last sequence update)  821-JUL-1986 (Rel. 01, Last sequence update)  822-JUL-1986 (Rel. 01, Last sequence update)  823-JUL-1986 (Rel. 01, Last sequence update)  823-JUL-1986 (Rel. 01, Last sequence update)  824-JUL-1986 (Rel. 01, Last sequence update)  825-JUL-1986 (Rel. 01, Last sequence update)
DECOURSE: OSTANDANDO OSTANDANDA OSTANDANDO OSTANDANDA OSTANDANDO OSTANDANDO OSTANDANDO OSTANDANDO OSTANDANDO OSTANDANDA OSTANDANDO OSTANDANDA OSTANDANDO OSTANDANDANDO OSTANDANDO OSTANDAND	EPO HUMAN STANDARD; PRT; 193 AA. PD 1589; O9UDZO; Q9UBAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, isst sequence update) 21-JUL-1986 (Rel. O1, isst sequence update) 21-JUL-1986 (Rel. O1, isst sequence update) ELYDAROPOGETIN precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Homo sapiens (Human) Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366; Jacobs K., Shoemaker C., Rudersdorf R., Neill S.D.,
DIOLOGY OND CONTRACTOR OF THE PROPERTY OF THE	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) ETYLAROPOICT (Rel. O1, Last amontation update) Brytharopoictin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINBE-861389366; MEDLINBE-861389366; MEDLINBE-861389366;
PULSES, OSUBZO, OSUBZO, OSUBAO, 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Mamwalia; Butheria; Chordata; Craniata; Vertebrata; Mamwalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDILINE=6817899; PubMed=3838366; MARINE-88177899; PubMed=383838966; MARINE-88177899; PubMed=3838366; MARINE-881789999; PubMed=3838966; MARINE-881789996; MARINE-881789996; MARINE-8817789996; MARINE-881789996; MAR	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; O9UHAO; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Isst sequence update) 21-UUL-1986 (Rel. O1, Isst sequence update) 21-UUL-1986 (Rel. O1, Isst sequence update) 81-UUL-1986 (Rel. O1, Isst sequence update) 821-UUL-1986 (Rel. O1, Isst sequence update) 822-UUL-1986 (Rel. O1, Isst sequence update) 823-UUL-1986 (Rel. O1, Isst sequence update) 823-UUL-1986 (Rel. O1, Isst sequence update) 824-1986 (Rel. O1, Isst sequence update) 825-UUL-1986 (Rel. O1, Isst sequence update) 825-UUL-1986 (Rel. O1, Isst sequence update) 825-UUL-1986 (Rel. O1, Created) 825-UUL-1986 (Rel. O1, Isst sequence update) 825-UUL-1986 (Rel. O1, Created) 825-UUL-198
DISBA: OBUDZO, OSTANDANO, PERIT, 193 AH. DISBA: OBUDZO, OSTANDANO, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 45, Last sequence update) Erythropictin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia, Eutheria, Primates, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, NCBI_TAXID=9606, SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366;	EPO HUMAN STANDARD; PRT; 193 AA. POISB8; OGUDZO; OGUEZS; OGUHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) 8 Erythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Fukaryota; Mamalla; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TAXID=9606; SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366;
PUISBS, OUNDZO, CATACACO, PARIS, 193 AH. PUISBS, OUNDZO, OTHERS, OSUHAO, 21-JUL-1986 (Rel. 01, Created) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; NCBI TaxID=9606; SEQUENCE FROM N.A. MEDIJNESBS17899; PubMed=3838366;	EPO HUMAN STANDARD; PRT; 193 AA. POJ BES QUUDZO; QUURZS; QUUHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Marazoa; Chordata; Craniata; Vertebrata; Mammanlais Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. MEDLINE=85137899; PubMed=3838366;
PULSEN, OSUDZO, OSUGNACO, PALIF, 193 AM.  21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last annotation update)	EPO HUMAN STANDARD; PDO HUMAN STANDARD; P01589; Q9UDZO; Q9UES; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE PROM NA. MEDIINEES117899: PihMed=3838366.
PULSES, OSUBZO, OSUBZO, OSUBAO, 21-7UL-1986 (Rel. 01, Created) 21-7UL-1986 (Rel. 01, Created) 21-7UL-1986 (Rel. 01, Last sequence update) 21-7UL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia; Cutheria; Crimiata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; [1] SEQUENCE FROM N.A. SERVING CRIMINIA (MAMINIDAE)	EPO HUMAN STANDARD; PRT; 193 AA. D1589, O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Humo sapiens (Human). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (1) SEQUENCE PROM N.A. SEQUENCE PROM N.A.
DOUGHANG OND OF THE PRINT	EPO HUMAN STANDARD; PRT; 193 AA. POT5 BB O HUMAN STANDARD; PUT5 9. 2015 BB; O 90 UDZ); QUUEZS; Q 9 UHAO; 21-3 UL-1986 (Rel. O1, Created) 21-3 UL-1986 (Rel. O1, Last sequence update) 21-3 UL-1986 (Rel. O1, Last sequence update) Erythxopoietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NEB TAXID=9606; SEQUENCE FROM N.A.
DISBA: OSUDZO; OSUGNACO; PELI; 193 AH.  21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) Brythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia; Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; SEQUENCE FROM N.A.	EPO HUMAN STANDARD; PRT; 193 AA. POT5 B9; 0905 B
DISBA: OSUDZO, OSUZONZO, OSUGARO, 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 45, Last amotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Mammalia; Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (I) [1] SEQUENCE PROM N.A.	EPO HUMAN STANDARD; PRT; 193 AA. POT589; O9UDZO: Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) 8Tythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human). Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, NCBI TaxID=9606; [1]. SEQUENCE PROM N.A.
D1588; O9UDZ0; O9UBZ25; O9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) Erythropietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Homo sapiens (Human). How sapiens (Human). How sapiens (Created Human). How Sapiens (Human). Success (Catarrhini; Hominidae, NCBI_TAXID=9606; Issupersor (Catarrhini; Hominidae, SEQUENCE FROM N.A.	EPO HUMAN STANDARD; PRT; 193 AA. POJ589; O9UDZO; Q9UEZS; Q9UHAO; 21-3UL-1986 (Rel. O1, Created) 21-3UL-1986 (Rel. O1, Created) 21-3UL-1986 (Rel. O1, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Homo sapiens (Human). Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutharia; Primates; Catarrhini; Hominidae; NCBI_TAXID=9606;   SEQUENCE FROM N.A.
DIOLOGY O 2010 CONTROL OF THIS TAY.  21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, East sequence update) EVALUACION (Rel. 45, Last annotation update) Name=EPO; Homo sapiens (Human). Fukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI TaxID=9606; INTILIATE PROM N b	BPO HUMAN STANDARD; PRT; 193 AA. P01589, Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) 8-Tythropoietin precursor (Epoetin). Name=EPO; Human). Eukaryota; Mutazoa; Chordata; Craniata; Vertebrata; Mammanlai; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606; Ill.
PULSES, OSUDZO, OSTATANO, PARIS, 193 AM. 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last annotation update) 21-UL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Nammalia, Eutheria, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, (1)	EPO HUMAN STANDARD; POIDS8; Q9UDZO; Q9UEZS; Q9UHAO; POIDS8; Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; NCBI TaxID=9666;
DOUGHAN OND OF THE PRINT T	EPO HUMAN STANDARD; PRT; 193 AA. D10589; 09UDZ0; Q9UBZ5; 09UHA0; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 01, East sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [1]
DOUBLE OF STANDARD, PARTY 193 AM.  21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin).  Name=EPO; Name=EPO; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [13]	EPO HUMAN STANDARD; PRT; 193 AA. POT589; O9UDZO; Q9UEZS; Q9UHAO; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, isst sequence update) 21-UUL-1986 (Rel. O1, isst sequence update) Erythxopietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NIS_TaxID=9606;
DISBN. OSUDORO, OSUBARO, ENT, 193 AH.  21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 45, Last sequence update) Erythropoietin precursor (Epoetin).  Name=EPO; Nome=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [11]	EPO HUMAN STANDARD; PRT; 193 AA. D1588; O9UDZO; Q9UEAC; Q9UEAC; Q9UEAC; 21-30L-1986 (Rel. O1, Created) 21-30L-1986 (Rel. O1, Created) 21-30L-1986 (Rel. O1, Last sequence update) 01-0CT-2004 (Rel. 45, Last annotation update) 8Tythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Howamalia; Eutheria; Primates; Catarrhini; Hominidae, NGE TaxID=9606;
D1588; O9UDZ0; O9UEZ5; O9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) Erythropietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human). (Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Ith	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO: Q9UEAG; Q9UEAG; Q9UEAG; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Last sequence update) 21-UUL-1986 (Rel. O1, Last sequence update) O1-CCT-2004 (Rel. 45, Last annotation update) Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Nell-TaxID=9606;
D10188; O9UDZ0, O9UEZ5, O9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last annotation update) Brythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammanlai; Eutheria; Primates; Catarrhini; Hominidae;	EPO HUMAN STANDARD; PRT; 193 AA. P01588; Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) 8-Tythopoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammanlai; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
PULSES, OSUDZO, OSTATANO, PARIT, 193 AH. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 01, Last annotation update) Name=EPO; Homo sapiens (Human). Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. NCBI TaxtD=9606;	EPO HUMAN STANDARD; POIS8; Q9UDZO; Q9UEZS; Q9UHAO; POIS88; Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI Tax1D=9606;
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DIOLOGY O CONTROL OF THE PRINT THE P	EPO HUMAN STANDARD; PRT; 193 AA. DOJŌSB; OSUDZO; QSUEZS; QSUHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) Erythropietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human). Chordata; Craniata; Vertebrata; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; McPI may Taynochot.
DOUGHAN OND OF THE PRINT OF THE	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last amnotation update) Erythxopoietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human). Homo sapiens (Human).
DISBN: OSUDORO, OSUBARO, 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 45, Last annotation update) Erythropictin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Fukaryots, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae,	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominiaee.
D10188; O9UDZ0; O9UEZ5; O9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Ammalia; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae:	EPO HUMAN STANDARD; PRT; 193 AA. P01589; O9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. O1, Last sequence update) O1-CCT-2004 (Rel. 45, Last annotation update) Name=EPO; Homo sapiens (Human). Homo sapiens (Human). Howo sapiens (Human). Howatzoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae:
D10188; O9UDZ0, Q9UEZ5, Q9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 45, Last annotation update) Erythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae.	EPO HUMAN STANDARD; POIS8, Q9UDZO; Q9UEZS; Q9UHAO; POIS88, Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Evalvaryota; Metazoa; Chordata; Craniata; Vertebrata; Evalvaryota; Mammalia; Eutheria; Primates: Catarrhin; Hominidae.
D10188; O9UDZ0, Q9UEZ5, Q9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Endatyota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Entherria: Privates. Catarrhin; Unminidae.	EPO HUMAN STANDARD; POT588; Q9UDZO; Q9UES; Q9UHAO; POT588; Q9UDZO; Q9UES; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
PULSES, OSUBZO, OSUBZA, OSUBAD, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 01-OCT-2004 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Home septions (Human). Examples (Human). Examples (Human). Examples (Homenand Chordata, Creanista, Vertebrata, Mammalia, Durith, Princella, Chordata, Creanista, Vertebrata, Mammalia, Durith, Princella, Chordata, Creanista, Vertebrata, Chordata, Chorda	EPO HUMAN STANDARD; PDI589, Q9UDZO; Q9UBAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia: Duthoropoietin precursor of the complex of
PULSES, OSUDZO, OSUBEZ, OSUGRA, PALI, 193 AM. 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Name=EPO; Elkaryota, Metazoa; Chordata; Craniata; Vertebrata;	EPO HUMAN STANDARD; POUD S09 OUDDS, GOURES; QOUHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
PULSES, OSUDZO, OSUBEZ, OSUGRA, PALI, 193 AM. 21-UL-1986 (Rel. 01, Created) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 01, Last sequence update) 21-UL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;	EPO HUMAN STANDARD; PD1589, Q9UDZO; Q9UBZS; Q9UHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
DOUBLE O OUDDEO, OSTATANO, PARI, 193 AM. 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo saplens (Human). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;	EPO HUMAN STANDARD; P01508; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, isst sequence update) 21-JUL-1986 (Rel. O1, isst sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Name=EPO; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
DISBN: OSUDORO, OSUBRANCO, ENTI, 193 AM. DISBN: OSUDORO, OSUBRAS, OSUBARO, 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 21-UUL-1986 (Rel. 45, Last annotation update) Erythropictin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukarvola: Metazoa: Chordata: Craniata: Vertebrata.	EPO HUMAN STANDARD; PRT; 193 AA. D1589; O9UDZO; Q9UEZS; O9UHAO; 21-JUL-1986 (Rel. O1, Created) 21-JUL-1986 (Rel. O1, Last sequence update) 21-JUL-1986 (Rel. 45, Last annotation update) Erythoropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human). Eukarvola: Metazoa: Chordata: Craniata: Verrebrata.
D101801, O9UDZ00, Q9UBZ5, Q9UHA0; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo sapiens (Human).	EPO HUMAN STANDARD; PRT; 193 AA. PO1588; O9UDZO; Q9UEZS; Q9UHAO; 21-UUL-1986 (Rel. O1, Created) 21-UUL-1986 (Rel. O1, Last sequence update) 01-CCT-2004 (Rel. 45, Last annotation update) Rrythropoietin precursor (Epoetin). Name=EPO; Home saplens (Human).
D10188; O9UDZ0, O9UEZ5, O9UHA0; 193 AH. 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, isst sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Name=EPO; Homo saplens (Human).	BPO HUMAN STANDARD; POT 5090 SUDDO: QOURES; QOUHAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-JUL-1986 (Rel. 01, Last sequence update) Erythropoietin precursor (Epoetin). Name=EPO; Homo saplens (Human).
POLSE 19 AND STANDARD POLSE 19 AND POLSE 19	EPO HUMAN STANDARD; POT589, Q9UDZO; Q9UBAO; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2004 (Rel. 45, Last annotation update) Erythropoietin precursor (Epoetin). Homo sapiens (Human).
21-JUL-1986 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet Name=EPO; Homo sapiens	EPO HUMAN PO1588; Q9UD 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet Name=EPO; Homo sapiens
21-7UL-1986 21-7UL-1986 21-7UL-1986 01-0CT-2004 Erythropoiet Name=EPO,	EPO HUMAN P01588; Q9UD 21-UUL-1986 21-UUL-1986 01-OCT-2004 Erythropoiet Name=EPO;
D1588, Q9UD 21-UUL-1986 21-UUL-1986 01-OCT-2004 Erythropoiet Name=EPO;	EPO HUMAN P01588; Q9UD 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet
ECT-1001 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet Name=EPO;	EPO HUMAN POL588; Q9UD 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet Name=EPO;
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ECT-000 21-001-1986 21-001-1986 01-0CT-2004 Erythropoiet	EPO HUMAN P01588; Q9UD 21-JUL-1986 21-JUL-1986 01-OCT-2004 Erythropoiet
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21-JUL-1986 21-JUL-1986 21-JUL-1986 01-OCT-2004	EPO HUMAN P01588; Q9UD 21-JUL-1986 21-JUL-1986 01-OCT-2004
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21-JUL-1986	EPO HUMAN P01588; Q9UD 21-JUL-1986
ECTIONAL STANDARD; P01588; Q9UDZO; Q9UEZS; Q9UHAO; 21-UH-1986 (Rel Ol Created)	EPO HUMAN STANDARD; POLESB; Q9UDZO; Q9UEZS; Q9UHAO; 21-JUL-1986 (Rel: 01. Created)
POLISES, QUUDZO, QUUEZS, QUUHAO,	EPO HUMAN STANDARD; PRT; 193 POLES; Q9UDZO; Q9UEZS; Q9UHAO;
P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;	EPO HUMAN STANDARD; PRT; 193 P01588; Q9UDZ0; Q9UEZ5; Q9UHA0;
P01588; O9UDZ0: O9UEZ5: O9UHA0:	EPO HUMAN STANDARD; PRT; 193 P01588; 09UDZ0; 09UEZ5; 09UHA0;
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WEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;

X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;

A Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
A Lhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
A Lhan H., Osslund T.D., Chirino A.J., Zhang J., Wendoloski J.J.,
A Eliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
A Egite J., Stroud R.M.;
A Egite J. Stroud R.M.;
A Egite J.M. NeoRecormon or Recormon and Procrit Corton Stroughly NeoRecormon or Recormon and Procrit Are Greek J. Variations in the Glycosylation pattern of EPO Corton Biotech). Variations in the Glycosylation pattern of EPO Corton Epoetin Deta and Epomax as epoetin of EPO Corton Recormon and Recormon as epoetin beta and Epomax as epoetin of EPO Corton Strough Str
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88153657; PubMed=3346214;
Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
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Takeuchi M., Kobata A.;
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/FIId=VAR 009870.
P -> Q (in an hepatocellular carcinoma).
/FIId=VAR 009871.
E -> Q (in Ref. 1; CAA26095).
Q -> QQ (in Ref. 5).
G -> R (in Ref. 1; CAA26095).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                            MIM; 133170; -...

Or. Go:0005615; P:response to stress; TAS.

GO; GO:0005515; P:response to stress; TAS.

InterPro; IPR009079; 4 helix cytokine.

InterPro; IPR003013; EPO TPO.

InterPro; IPR003013; EPO TPO;

PEM; PER00758; EPO TPO; 1.

PRINTS; PR00272; ERYTHROPTN.

PROSITE; PS00817; EPO TPO; 1.

3D-structure; Direct protein sequencing; Erythrocyte maturation; Glycoprotein; Hormone; Pharmaceutical; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                Removed in mature form (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.2%; Score 851; DB 1; Length 193; 100.0%; Pred. No. 1.4e-71; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                           O-linked (GalNAc. .).
SL -> NF (in an hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21306 MW; C91F0E4C26A52033 CRC64;
                                                                                                                                                                                                                                                                                                        N-linked (GlCNAC. ..).
FTIG=CAR 000052.
N-linked TGLNAC. ..).
FTIG=CAR 000166.
N-linked (GlCNAC. ..).
FTIG=CAR (GlCNAC. ..).
O-linked (GlCNAC. ..).
                                                                                                                                                                                                                                                                        Erythropoletin.
                                                                                                                                                                                                                                                                                                                                                                             carcinoma).
            AF2023356; AAC787911; AF202308; AAC787911; AF202306; AAF23132.1; JOINED.; AF202307; AAF23133.1; JOINED.; AF202309; AAF23133.1; JOINED.; AF202309; AAF23133.1; JOINED.; AF202311; AAF17572.1;
                                                                         AF202312; AAF23134.1; JOINED.
AF202313; AAF23134.1; JOINED.
S65458; AAD13964.1; -
00.855. 7777.
                                                                                                                  PDB; 1BUY; NMR; A=28-193.
PDB; 1CN4; X-ray; C=28-193.
PDB; 1EER; X-ray; A=28-193.
GlycoSuiteDB; P01588; --
Genew; HGNC:3415; EPO.
MIM; 133170; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                 27
193
193
188
60
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                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                           A01855; ZUHU.
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EMBL; X02158; CAA26095.1; -.

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192 AA.
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InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR003013; Erythroptn.
Pfam; PP00758; EPO TPO; I.
PIRSF; PIRSF001951, EPO; 1.
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PROSITE; PS00817; EPO_TPO; 1
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                                                                                                               Erythropoietin precursor.
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152; Conservative
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152
192 AA;
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                                                                                                                                                                                                                                                       NCBI_TaxID=9541;
                                                                                                                                     Name=EPO;
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CARBOHYD
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Matches
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                                                                                                   VEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                   69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                         68
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            APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                        193
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Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T.,
"The sequence of Homo sapiens BAC clone RP11-336D7.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 851; DB 2; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walerston R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009488; AAP22357.1; -.
Hypothetical protein.
SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.H.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Toward a complete human genome sequence."; Genome Res. 8:1097-1108(1998).
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MEDLINE=99063792; PubMed=9847074;
                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.2%;
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Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
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AAP22357;
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Homo

RESULT 2
AAP22357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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similarity).
similarity).
                                                                                                                            Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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(By
(By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.
By similarity.
N-linked (GloNAc...) (1
N-linked (GloNAc...) (1
N-linked (GloNAc...) (1
O-linked (GalNAc...) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and by liver of fetal or neonatal mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.1%; Score 769.5; DB 1 91.6%; Pred. No. 6.1e-64; ive 7; Mismatches 6
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity.
Erythropoietin.
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Erythropoletin.
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P33708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=EPO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                     Q867B1
                                RESULT 5
Q867B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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셤
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 APPRLVCDSRVLERYLLEAKEAENVTMGCSESCSLNENITVPDTKVNFYAWKRIEVGQQA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
MCBI_TaxID=9544;
                                                                                                                                                            TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
MEDLINE=93372347; PubMed=8364201;
Czelusniak J., Goodman M., Eunn H.F.,
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 764.5; DB 1
Pred. No. 1.8e-63;
                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
              PRT;
                                                                                                                                                                                                                   sequence homology among mammals."; Blood 82:1507-1516(1993).
                                                                                     Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.5%;
90.4%;
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                                                                  Erythropoietin precursor.
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
65
110
152
192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 150; Conserv
                                                                                                                                                     SEQUENCE FROM N.A.
              EPO MACMU
                                                                            Name=EPO:
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69 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
Kijima-Suda I.;
"Nucleotide sequence of equine erythropoietin and characterization of
region-specific antibodies.";
Am. J. Vet. Res. 65:15-19(2004).
EMBL; AB100030; BAC55239.1;
HSSP; P01588; 1BUY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eguus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Eguus.
NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPDAASAAPLRTFAVDTLCKLFRIYSNFLRGKLKLYTGEACRRGDR 192
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129 PPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
                                                                                    147 LPDAASAAPLRTITADTFCKLFRVYSNFLRGKLKLYTGEACRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:000557; C:extracellular; IEA.
GO; GO:0005128; F:erythropoietin receptor binding; IEA.
GO; GO:0005129; F:hormone activity; IEA.
GO; GO:0005179; F:hormone activity; IEA.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001323; EPO TPO.
InterPro; IPR00131; EPYThroptn.
Pfam; PF00758; EPO TPO; 1.
PRINTS; PRSF001951; EPO: 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO TPO; 1.
SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 141; Conservative
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PubMed=14719696;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley; TISSUB-Kidney;
MEDLINE-93372347; PubMed=8364201;
Men D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
Acodman M., Bunn H.F.;
"Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
Blood 82:1570-1516(1993).
"C -1- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.

-1- SUBCELLULAR LOCATION: Secreted
-1- TISSUB SPECIFICITY: Produced by kidney or liver of adult mammals
-1- TISSUB SPECIFICITY: Produced by Ridney or liver of adult mammals
-1- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                 Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 APPRLICDSRVLERYILEAKEAENVTMGCAEGPRLSENITVPDTKVNFYAWKRKVEEQA
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N-linked (GlonAc. . .) (By similarity)
N-linked (GlonAc. . .) (By similarity)
N-linked (GlonAc. . .) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 706; DB 1; Length 192; 82.5%; Pred. No. 5.5e-58;
                                                                                                                                                                                                                                                                                      Nagao M., Suga H., Okano M., Masuda S., Narita H., Ikura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
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                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence of rat erythropoietin."; Biochim. Biophys. Acta 1171:99-102(1992).
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RGD; 2559; Epo.
InterPro; IPR001079; 4 helix cytokine.
InterPro; IPR001023; Epo TPO.
InterPro; IPR003013; Erythroptn.
PERR; PR0778; EPO TPO; 1.
PIRSF; PR067019; EPO TPO; 1.
PRNSF; PR067019; EPO TPO; 1.
PRNSF; PR067019; EPO TPO; 1.
PRNSF; PR067019; EPO TPO; 1.
                                                                                                                                                                                                                                  STRAIN-Wistar; TISSUE-Kidney;
MEDLINE-93042015; PubMed=1420369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21286 MW;
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Matches 137; Conservative
Erythropoietin precursor
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192
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109
192 AA;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Blood 82:150-1516(1993).
-!- FUNCTION: Brythroppietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-!- SUBCELUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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By similarity.
By similarity.
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
T (in Ref. 2).
                                                                                               SEQUENCE OF 5-192 FROM N.A.
MEDLINE=9372347; PubMed=8364201;
Wen D., Boissel J.P.R., Trayn E., Gruninger R.H., Mulcahy L.S.,
Czeluaniak J., Goodman M., Burn H.F.,
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 711; DB 1; Length 192;
Pred. No. 1.9e-58;
9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
            Goodman R.E., Bell R.G.,
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G -> E (in Ref. 2).
61C5EA0F5E937293 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR003013; EPO TPO.
InterPro; IPR03013; EPO TPO.
PERSF; PERSF001951; EPO; 1.
PRNTS; PR00272; ERYTHROPIN.
PROSITE; PS00817; EPO TPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequ
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 G
20914 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.5
Best Local Similarity 83.7
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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CONFLICT
SEQUENCE
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68 98

129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174

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Last sequence update) Last annotation update)

RESULT 7
EPO RAT
ID EPO
AC P29
DT 01DT 01DT 05-

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**O6PWUS** RESULT 8 QEPWUS ID QEPW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRAIN-Boran, TISSUE-Kidney;

C TRAIN-Boran, TISSUE-Kidney;

C TRAIN-Boran, TISSUE-Kidney;

Majiwa P.A.O., Feldman B.F., Mertens B.,

Logan-Henfrey L.L.;

A Logan-Henfrey L.L.;

C Ichning of a cDNA encoding bovine erythropoietin and analysis of its

T "Cloning of a cDNA encoding bovine erythropoietin and analysis of its

T "Cloning of a cDNA encoding bovine erythropoietin and analysis of its

T "Cloning of a cDNA encoding bovine erythropoietin in the regulation. In selected tissues.",

Gene 171:275-280(1996).

T "FUNCTION: Erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

C Physiological level of circulating erythrocyte mass.

T SUBCELULAR LOCATION: Secreted.

C -- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of feat or neonatal mammals.

C -- SIMILARITY: Belongs to the EPO / TPO family.
41 APPRLICDSRVLERYILEAREAENVTMGCAQGCSFSENITVPDTKVNFYTWKRMDVGQQA 100
                                                                                         VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin.

By similarity.

By similarity.

N-linked (GICNAC...) (Potential).

N-linked (GICNAC...) (Potential).

N-linked (GICNAC...) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.0%; Score 697.5; DB 1; Length 192; 83.2%; Pred. No. 3.4e-57;
                                                                                                                                                                            161 LPEEASPAPIRTFTVDTLCKLFRIYSNFLRGKLTLYTGEACRRGDR 206
                                                                                                                                                     129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DBC419022F7B483A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00758; BED TP0; 1.
PIRSF; PIRSF001951; EPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO TPO; 1.
Brythrocyte maturation; Glycoprotein; Hormone; Signal.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001323; BPO TPO.
InterPro; IPR003013; Brythroptn.
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                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L41354; AAB41268.1; -. EMBL; U44762; AAA86653.1; -. HSSP; P01588; ICN4.
                                                                                                                                                                                                                                                                                                                                                                                                                  Erythropoietin precursor.
                                                                                                                                                                                                                                                                                                         STANDARD;
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192
187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovinae; Bos
                                                                                                                                                                                                                                                                                                         EPO BOVIN
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DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                 RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LEVWOGLALLSEAILRGOALLANASOPSETPOLHVDKAVSSLRSLTSLLRALGAOKEAMS 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis fâmiliaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Rissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
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Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.;
Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.;
"Description of the full length of canine erythropoietin.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AX572971; AS577874.1; --
SEQUENCE 206 AA; 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match

78.1%; Score 698; DB 2; Length 206;
Best Local Similarity 81.3%; Pred. No. 3.4e-57;
Matches 135; Conservative 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.1%; Score 698; DB 2; Length 206; Best Local Similarity 81.3%; Pred. No. 3.4e-57; Matches 135; Conservative 13; Mismatches 18; Indels
161 LPEEASPAPLRTFTVDTLCKLFRIYSNFLRGKLTLYTGEACRRGDR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                              Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYS72971; AAS77874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001332; EPO TPO.
Ffam; PF00758; EPO TPO; 1.
PRINTS; PR00272; ERYTHROPIN.
PROSTIE; PS00817; EPO TPO; 1.
SEQUENCE 206 AA; 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Erythropietin.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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15-APR-2004 (TrEMBLrel. 27, Last seq
15-APR-2004 (TrEMBLrel. 27, Last anno
                                                                                                                                                                              Created)
                                                                                                                                                                              05-JUL-2004 (TrEMBLrel, 27,
                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adult sheep.
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CARBOHYD
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                                                                                                                                                            69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                 68
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                                                                    9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Abnormal erythropoietin (Epo) gene expression in the murine erythroleukemia IW32 cells results from a rearrangement between the G-protein beta subunit gene and the Epo gene."; Oncogene 15:1995-1999(1997).

- FUNCTION: Brythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miller W., Koop B.F., "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5. Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87039105; PubMed=3773894;
Shoemaker C.B., Mitsock L.D.;
"Murine erythropoietin gene: cloning, expression, and human gene
    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129/Sv;
MEDLINE=21138439; PubMed=11239002;
Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87039104; PubMed=3022133;
McDonald J.D., Lin F.-K., Goldwasser E.;
"Cloning, sequencing, and evolutionary analysis of the mouse
                                                                                                                                                                                                                                   174
    19; Indels
                                                                                                                                                                                                                                                   146 LPDATPSAAPLRAFTVDALSKLFRIYSNFLRGKLTLYTGEACRRGDR
                                                                                                                                                                                                                            129 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          192 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology.";
Mol. Cell. Biol. 6:849-858(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98030528; PubMed=9365246;
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139; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erythropoietin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 07, (Rel. 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erythropoietin gene.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1988
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                        EPO MOUSE
P07321;
Matches
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
       no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 APPRIICDSRVLERYILEAKEAENVTMGCAEGPRLSENITVPDTKVNFYAWKRMEVEEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).
(By similarity).
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.; "The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
     is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
Wen D., Boissel J.P.R., Tracy T.B., Gruninger R.H., Mulcahy L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 192;
   as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 PPDTTPPAPLRTLTVDTFCKLFRVYANFLRGKLKLYTGEVCRRGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65F94E214E0DEF2E CRC64;
                                                                                                                                                                                                                                                                                                   PRINTS; PR00272; ERYTHROPIN.
PROSITE; PS00817; EPO TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                              By similarity.
N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 694; DB 1;
Pred. No. 7.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P33709; 028572;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               Erythropoletin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 AA
institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Cell. Endocrinol. 93:107-116(1993)
                                                                                                                                                                                         MEST, MI:95407, EDO.
INTERPRO, IPR009079; 4 helix cytokine.
INTERPRO, IPR001323; EPO TPO.
INTERPRO, IPR003013; Erythroptn.
Pfam; PP00758; EPO TPO; 1.
PIRSF; PIRSF001951; EPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Kidney;
MEDLINE=93351736; PubMed=8349021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21365 MW;
                                                                                                                          EMBL; AF312033; AAK28825.1; -
EMBL; Y11971; CAA72707.1; -.
PIR; A24902; A24902.
                                                                                       EMBL; M12482; AAA37568.1; -. EMBL; M12930; AAA37570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.1
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erythropoietin precursor
                                                                                                                                                                                                                                                                                                                                                            26
192
187
50
64
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89 VEVWQGLALLSEAMIRSQALLANSSQLPETLQVHVDKAVSGLRSLTSLIRALGVQKEAVS 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 APARLICDSRVLERYILEAKEAENVTMGCAEGCSLGENITVPDTKVNFHHWKKSEAGRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolāgus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 76.7%; Score 685.5; DB 2; Length 195; Best Local Similarity 81.4%; Pred. No. 4.7e-56; Matches 136; Conservative 12; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 685.5; DB 2; Length 195; Pred. No. 4.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 PPEAASSAAPLRTVAADTLCKLFRIYSNFLRGKLKLYTGEACRRGDR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005128; F: erythropoietin receptor binding; IEA.
GO; GO: 0005129; F: hormone activity; IEA.
GO; GO: 0005179; F: hormone activity; IEA.
InterPro; IPR001023; EPO TPO.
InterPro; IPR001033; EPO TPO.
InterPro; IPR001031; EPO TPO: 1.
Pfam; PF00758; EPO TPO: 1.
PRINTS; PR00272; ERYTHROPIN.
PROSITE; PS00817; EPO TPO: 1.
PROSITE; PS00817; EPO TPO: 1.
SEQUENCE 195 AA; 21053 MW; 0999DA7D852713F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=21290682; PubMed=11396976;
Vilalta A., Wu D., Margalith M., Hobart P.;
Vilalte Bro gene and cDNA: expression of rabbit EPO after intramuscular injection of pDNA.";
Biochem. Biophys. Res. Commun. 284:823-827(2001).
EMBL; AF290943; ARG36961.1; -.
PIR; JC7699; JC7699.
                                                                                                                                                                              A MASS, FOLDS 84; LLN4.

GO; GO:00055128; F:erythropoletin receptor binding; IBA.

GO; GO:0005129; F:hormone activity; IEA.

GO; GO:0005179; F:hormone activity; IEA.

InterPro; IPR001323; EFO TPO.

InterPro; IPR001323; EFO TPO.

InterPro; IPR001313; EFO TPO.

INTERPRO; PROSTO 13; EFO TPO.

INTERPRO; PROSTO 15; EFO TPO; 1.

PERMINS; PR00272; ERYTHROPIN.

PRENTS; PR00272; ERYTHROPIN.

PROSITE; PS00017; EPO TPO; 1.

SEQUENCE 195 AA; 21025 MW; IFIDC7F403A303EC CRC64;
                   MEDLINE=21290682; PubMed=11396976;
Vilalta A., Wu D., Margalith M., Hobart P.;
Rabbit EPO gene and cDNA: expression of rabbit EPO after
intramuscular injection of pDNA.";
Biochem. Biophys. Res. Commun. 284:823-827(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                     Biochem. Biophys. Res. Commun.
EMBL; AF290944; AAG36962.1; -.
HSSP; P01588; 1CN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.7%;
81.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01588; 1CN4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erythropoietin.
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                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 LEVWQGLALLSEAIFRGQALLANASQPCBALRLHVDKAVSGLRSLTSLLRALGAQKEAIP 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Czelusniak J., Goodman M., Bunn H.F.;
"Brythopolicatin structure-function relationships: high degree of
"Brythropolicatin structure ammals.";
Blood 82.1507-1516(1993)
"In mammals.";
FUNCTION: Erythropoletin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of
physiological level of circulating erythrocyte mass.
                                                                                                                                                                    -:- SUBCELLUIAR LOCATION: Secreted.
-:- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-:- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By similarity.

Expthropoletin.
By similarity.
By similarity.
N'linked (GloNAc. .) (Pote N-linked (GloNAc. .) (Pote N-linked (GloNAc. .) (Pote N-linked (GloNAc. .) (Pote F - L (in Ref. 2).
L - P (in Ref. 2).
L - P (in Ref. 2).
W, CO25AABO528131A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Exythropoietin.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.6e-56;
9; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 690.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; 146401; 146401.
HSSP; 901588; 1CM4.
InterPro; 1PR003079; 4 helix_cytokine.
InterPro; 1PR001323; EPO_TPO.
InterPro; 1PR003013; EPV—TPO.
Pfam; PP00758; EPO_TPO; 1.
PfSF; PIRSP01951; EPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21335 MW;
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82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z24681; CAA80848.1; -. EMBL; L10610; AAA31518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.0
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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194
189
60
51
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
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RESULT 13 Q9GKA2

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qq ð

8

89

Gaps

ij

NATERIAL MANAGEMENTS NATERAL SOLUTION NA

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TISSUE-Kidney,

MEDLINE-93372347; PubMed=8364201;

MEDLINE-93372347; PubMed=8364201;

Med D., Boissel J. P. R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,

A Wen D., Boissel J. Tracy T.E., Gruninger R.H., Mulcahy L.S.,

Caeluaniak J., Goodman M., Bunn H.F.;

Encludiak J., Goodman M., Bunn H.F.;

Encludiak J. Struction and Tracy T.E., Gruninger R.H., Mulcahy L.S.,

Encludiation Server-function relationships: high degree of a requestion of erythrocote differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

C. I- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

C. I- SUBCELLULAR LOCATION: Secreted.

C. I- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.

C. I- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                     VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                   PPDAA-SAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
                                                                                                                                                                                        18; Indels
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By similarity.
By similarity.
N-linked (GlcNAc. .) (Pott.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; 146578; 146578.
HISSP, PO1588; 1074.
InterPro; IPR003079; 4 helix cytokine.
InterPro; IPR00313; EPC_TPO.
InterPro; IPR003013; EYThroptn.
Pfam; PF00758; EPO TPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO TPO; 1.
Brythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                          190 AA.
   12; Mismatches
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190 Er
185 By
46 N-
60 N-
168 N-
20888 MW,
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01-FEB-1996 (Rel. 33, Last seq
05-UUL-2004 (Rel. 44, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L10607; AAA31029.1; -.
Matches 136; Conservative
                                                                                                                                                                                                                                                                                        STANDARD;
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190 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
                                 6
                                                                                                    69
                                                                                                                                                                   129
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                                                                                                      23 APPRLICDSRVLERYILEAKEGENATMGCAESCSFSENITVPDTKVNFYAWKRMEVQQQA 82
                                                                      APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                            Gaps
                                        2;
                                                                                                                                                                                                                               143 LPDASPSSATPLRTFAVDTLCKLFRNYSNFLRGKLTLYTGEACRRRDR 190
        Length 190;
                                                                                                                                                                                                        129 PPDA--ASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                        Indels
     Score 683; DB 1; L. Pred. No. 7.8e-56; 7; Mismatches 21;
     76.4%;
82.1%;
Query Match
Best Local Similarity 82.1<sup>5</sup>
Matches 138; Conservative
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completed: November 19, 2004, 21:10:58

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search,

November 19, 2004, 20:57:38 ; Search time 59.4932 Seconds (without alignments) 1019.028 Million cell updates/sec Run on:

US-10-014-363-4

Perfect score: ritle:

1 APPAPPRLICDSRVLERYLL.....NFLRGKLKLYTGEACRTGDR 169 Sequence:

BLÓSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* A\_Geneseq\_23Sep04:\* 1: qenesem1000-

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Abb77899 Amino aci	2 Amino	Amino	Amino		Amino	$\overline{}$	æ	93	4	O Human	0 Modifi	Abb83622 Protein #	Aae02641 Human ery		Abg92101 Human ery	Human	7 Amino	Adg65661 Human ery	6 Human	0 Human	9 Human	- 1	4	7 Human
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Adl06781 Human 166	Ado59416 Human 166	Aap50299 Human rec	Aap50298 Human rec		Erythr			_		Aar71137 Human ery		Aar81982 Human ery	Aar98397 Human ery	Aay43398 Human ery	Aay94530 Human ery	Amino		Aab34978 Human erv	Aab85573 Human ery
ADL06781	AD059416	AAP50299	AAP50298	AAP60599	AAP81195	AAP50300	AAP60597	AAP70256	AAR65499	AAR71137	AAR74141	AAR81982	AAR98397	AAY43398	AAY94530	AAY93638	AAY99704	AAB34978	AAB85573
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97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production, anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor. Amino acid sequence of a modified human erythropoietin (EPO). ABB77899 standard; protein; 169 AA. (first entry) 07-OCT-2002 ABB77899; 

Homo sapiens. Synthetic.

 .3 /note= "proteolytic cleavage site" /note= "EPO protein" Location/Qualifiers 4. .174 WO200249673-A2. Cleavage-site Protein

08-DEC-2001; 2001WO-EP014434. 27-JUN-2002.

20-DEC-2000; 2000EP-00127891.

(HOFF ) HOFFMANN LA ROCHE & CO AG F.

3 Tischer Schurig HE, Hilger B, Engel A, Franze R, Burg J, Wozny M;

WPI; 2002-566640/60.

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

Disclosure, Page 39; 40pp; English.

The present sequence represents a modified human erythropoietin (EPO) protein. The BPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The

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specification describes a conjugate comprising an EPO glycoprotein having
          an N-terminal alpha-mailno group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycosylation sites covalently linked to a poly(ethylation site). The glycoprotein is bas in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anomenia in chronic renal failure patients (CRF), acquired numdergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid
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                                                                                                                                                                                                                                                                                                               Score 869; DB 5;
Pred. No. 8.1e-88;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB77902 standard; protein; 196 AA.
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                                                                                                                                                                                                                                                progenitors in the bone marrow
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Best Local Similarity 100.0%;
Matches 169; Conservative 0
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/note= "F
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                                                                                                                                                                                                                                                                                   Sequence 169 AA;
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The present sequence represents a modified human erythropoietin (EPO)

protein. The EPO was extended at the N-terminal by a proteolytic cleavage
site. It was used to produce conjugates of the invention. The
specification describes a conjugate comprising an EPO glycoprotein having
an N-terminal alpha amino group, chosen from human EPO (hEPO) or its
analogues (where hEPO is modified by addition of 1-6 glycosylation sites
or a rearrangement of a glycosylation site). The glycoprotein sites
or are rearrangement of a glycosylation site). The glycoprotein sites
or are invivo biological activity of causing bone marrow cells to increase
production of reticulocytes and red blood cells. The conjugate increased
circulating half-life and plaama red blood cells. The conjugate increased
circulating half-life and plaama red blood cells. The conjugate increased
circulating half-life and plaama red blood cells. The conjugate increased
circulating the file EPO. The EPO conjugate is useful for preparing
medicaments for the treatment and prophylaxis of diseases correlated with
anaemia in chronic renal failure patients (CRF), acquired
compared to windome (AIDS) and for treating cancer patients
cundergoing chemotherapy. It is also useful for treating patients by
stimulating the division and differentiation of committed erythroid
compared to the properties of committed erythroid
compared to marrow
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                                                                                            gate of erythropoietin glycoprotein with polyethylene glycol, treating diseases correlated with anemia in chronic renal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 869; DB 5; Length 1:
100.0%; Pred. No. 1e-87; wiematches 0; Indels
                                                                                                                                           failure patients and acquired immunodeficiency syndrome.

    .8
/note= "proteolytic cleavage site"

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/note= "EPO protein"
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                                   WPI; 2002-566640/60.
                                                                                                       conjugate of
                                                           N-PSDB; ABL59290
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Location/Qualifiers 1. .8 /note= "proteolytic cleavage site"

/note= "EPO protein"

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56 RMEVGOQAVEVWQGIALLSEAVLRGQALLVNSSQPWEPLQLHVDXAVSGLRSLTTLLRAL 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.6%; Score 856.5; DB 5; Length 174; Best Local Similarity 97.1%; Pred. No. 2e-86; Matches 169; Conservative 0; Mismatches 0; Indels 5
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                                                                                                                                            WPI; 2002-566640/60.
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Best Local Similarity
                                                                                                              Engel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 174 AA;
          WO200249673-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-2002
                              27-JUN-2002
                                                                                                              Burg J,
Wozny M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB77900;
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Novel conjugate of erythropoietin glycoprotein with polyethylene useful for treating diseases correlated with anemia in chronic refailure patients and acquired immunodeficiency syndrome.
acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                       committed erythroid progenitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2000; 2000EP-00127891
                                                                                                                                                                                                                                                                                                                                                                                                                                                         38-DEC-2001; 2001WO-EP014434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-566640/60.
                                                                                                                                                                                                                                                                                                                                           WO200249673-A2
                                                                                                                                                                                                  Cleavage-site
                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-2002
                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burg J,
Wozny M;
The present sequence represents a modified human erythropoietin (EPO)

protein. The EPO was extended at the N-terminal by a proteolytic cleavage

site. It was used to produce conjugates of the invention. The

specification describes a conjugate comprising an EPO specification describes a conjugate comprising an EPO specification having

an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its

an N-terminal alpha-amino group, chosen from human EPO specification sites

or a rearrangement of a glycosylation site). The glycopyrotein is

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein

covalently linked to a poly(ethylene glycol) group.

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covalently linked to a glycopy 
                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycol,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel conjugate of erythropoietin glycoprotein with polyethylene gly useful for treating diseases correlated with anemia in chronic renal fallure patients and acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                          Tischer W;
                                                                                                                                                                                                                                                                                                       Schurig HE,
                                                                                                                                                                                                                                                                                                          m
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 38-39; 40pp; English.
                                                                                                                                                                                                                                                                                                 Hilger
                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             progenitors in the bone marrow
                                                                                                                                                                                                                                                                                                       Franze R,
                                                                                                                             08-DEC-2001; 2001WO-EP014434
                                                                                                                                                                                      20-DEC-2000; 2000EP-00127891
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Tischer W;

Schurig HE,

Hilger B,

Engel A, Franze R,

The present sequence represents a modified human erythropoietin (BPO)

Strotein. The EPO was extended at the N-terminal by a proteolytic cleavage

site. It was used to produce conjugates of the invention. The

specification describes a conjugate comprising an EPO specification describes a conjugate comprising an EPO specification describes a conjugate comprising an EPO specification are specification describes a conjugate comprising an EPO specification by addition of 1-6 specification sites

or a rearrangement of a glycosylation site. The glycosylation sites

or a rearrangement of a glycosylation site. The glycopylation sites

or a rearrangement of a glycosylation site. The glycopylation sites

covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein is

covalently linked to a poly(ethylene glycol) group. The EPO glycopylation sites

covalently linked to a poly(ethylene glycol) group. The EPO conjugate increased

circulating half-life and plasma residence time, decreased clearance,

circulating half-life and plasma residence (ERE), acquired

medicaments for the treatment and prophylaxis of diseases correlated with

medicaments for the treatment and prophylaxis of diseases correlated with

immunodeficiency syndrome (AIDS) and for treating patients

maemic and planting the division and differentiation of committed erythroid ij 115 61 RMEVOQQAVEVWQGLALLSBAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120 09 55 1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTKVNFYAWK 56 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 1 APP-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK Gaps 116 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169 121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174 2 Length 174; Indels 5; 0 Score 856.5; DB Pred. No. 2e-86; 0; Mismatches Disclosure; Page 39-40; 40pp; English in the bone marrow Query Match 98.6%; Best Local Similarity 97.1%; Matches 169; Conservative Sequence 174 AA; progenitors 셤 ઠે a ઠે g

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Indels

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CC protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The EPO was extended conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (BEDO) or its analogues (where hEPO is modified by addition of 1-6 glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein of as in vivo biological activity of causing bone marrow cells to increased correlation of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anamania in chronic remal failure patients (CRF), acquired immunosficient elements of correlated with confidence of the EPO supply of the EPO supplying cancer patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             undergoing chemotherapy. It is also useful for treating patients stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
                                                                                                                                                Human, erythropoietin, EPO; glycoprotein, reticulocyte production, red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tischer W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.6%; Score 856.5; DB 5; Length 201; 97.1%; Pred. No. 2.5e-86; ive 0; Mismatches 0; Indels 5;
                                                                                                                 Amino acid sequence of a modified human erythropoietin (EPO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schurig HE,
                                                                                                                                                                                                                                                                                                                                                         "proteolytic cleavage site"

    .27
    note= "secretion signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG F.
                                                                                                                                                                                                                                                                                                                                                                                         /note= "EPO protein"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
              ABB77901 standard; protein; 201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 40pp; English.
                                                                                                                                                                                                     committed erythroid progenitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LA ROCHE & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2001; 2001WO-EP014434
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                                                                                   entry)
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N-PSDB; ABL59289.
                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                            WO200249673-A2
                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-2002
                                                                                                                                                                                                                                       Synthetic
                                              ABB77901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burg J,
Wozny M;
                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                           Protein
ABB77901
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Gaps

5.

Best Local Similarity 97.1 Matches 169; Conservative

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The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an EPO 91ycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein has in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when
                                                                       115
                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
 55
                                 87
                                                                   56 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
                                                                                            88 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
1 APP----APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDIKVNFYAWK
                                 28 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDIKVNFYAWK
                                                                                                                                             GAQKBAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                              Human, erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tischer W;
                                                                                                                                                                 148 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a modified human erythropoletin (EPO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schurig HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "proteolytic cleavage site"
36. .201

    27
    note= "secretion signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "EPO protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                           Α̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 40pp; English
                                                                                                                                                                                                                                                                           ABB77903 standard; protein; 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-2001; 2001WO-EP014434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-DEC-2000; 2000EP-00127891
                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL59291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                ABB77903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burg J,
Wozny M;
                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                         RESULT 6
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RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 115
                                                                                                                                                                                                                                                                                                            55
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medicaments for the treatment and prophylaxis of diseases correlated anamenia in chronic renal failure patients (CRF), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients stimulating the division and differentiation of committed erythroid progenitors in the bone marrow
                                                                                                                                                                                                                                                          APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                             1 APP----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                                                                                                                                                                     GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                      Length 201;
                                                                                                                                                                                                   Indels
                                                                                                                                                                   Score 856.5; DB 5;
Pred. No. 2.5e-86;
0; Mismatches 0;
                                                                                                                                                                   98.6%;
97.1%;
                                                                                                                                                                                              Matches 169; Conservative
                                                                                                                                                                                Local Similarity
                                                                                                                                     Sequence 201 AA;
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                                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                  Query Match
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Non-glycosylated EPO analogue with modified protease B signal peptide. Ä ADJ71846 standard; protein; 205 (first entry) 06-MAY-2004 ADJ71846; RESULT 7 

non-glycosylated erythropoietin analogue; EPO analogue; PEG; anaemia; protease B signal peptide. /note= "Modified protease B signal peptide region" Location/Qualifiers .39 Key Misc-difference Synthetic. Unidentified. Chimeric

WO2004009627-A1

.205 :e= "Non-glycosylated BPO analogue region"

/note=

Misc-difference

29-JAN-2004

17-JUL-2003; 2003WO-CA001020.

19-JUL-2002; 2002US-0396750P

(CANG-) CANGENE CORP

Stewart Malek LT, Cossar JD,

2004-214326/20. N-PSDB; ADJ71845 non-glycosylated erythropoietin (BPO) analog useful treating anemia, here the lysine at position 45 and/or 116 has been replaced with an nino acid that cannot be pegylated. amino

immature megakaryocyte. Human EPO effects megakaryocyte-platelet system other than an erythrocyte growth effect. Megakaryocyte-platelet growth is usable as a remedy for diseases caused by a platelet decrease

Length 166;

97.9%; Score 851; 100.0%; Pred. No.

Query Match Best Local Similarity

A.

All of the Cys residues in the SQ are labelled "SH". Megakaryocyteplatelet growth factor contains human EPO as an active principle. Human EPO has a megakaryocyte colony-stimulating activity and increases the ratio of small acetyl cholinesterase posititive cell (SAchE+) which is

Disclosure, Page 181; 8pp; Japanese.

platelets

74pp; English. Disclosure; SEQ ID NO 29;

The invention comprises the amino acid and coding sequences of non-glycosylated erythropoietin (EPO) analogues, where the lysine at position

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45 and/or 116 has been replaced with an amino acid that cannot be pey/lated. The non-glycosylated EPO analogues of the invention are useful for treating anaemia. The present amino acid sequence represents a non-glycosylated EPO analogue with a modified protease B signal peptide. NOTE: The present sequence is included in the sequence listing as SEQ ID No 29, however another sequence on page 28 of the specification is also shown as SEQ ID No 29.
                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Megakaryocyte-platelet growth factor - contains as active component human erythropoietin and is used to treat diseases caused by decrease in
                                                                                                                                                                                                               96
                                                                                                                                                                                                    1 APPAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVG
                                                                                                                                                                                                                                     61 QQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mega-karyocyte-platelet growth factor; hormone;
mega-karyocyte colony stimulating factor; therapy;
small acetyl cholinesterase positive cell; erythrocyte growth effect.
                                                                                                                                                              Gaps
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0
                                                                                                                                                                                                                                                                                                       121 AISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                  Length 205
                                                                                                                               Score 853; DB 8; L
Pred. No. 6.4e-86;
3; Mismatches 2;
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of human erythropoietin (EPO)
                                                                                                                                                                                                                                                                                                                                                                                   Ą.
                                                                                                                                                                                                                                                                                                                                                                               AAP70398 standard; protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86JP-00191542.
                                                                                                                               Query Match
Best Local Similarity 98.8%;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85JP-00203049.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1987-224837/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAWA/) KAWAKITA
                                                                                                        Sequence 205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP62149624-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-1987.
                                                                                                                                                                                                                                                                                                                                                                                                          AAP70398;
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                                                                                                                                                                                                                                                                                                                                                     RESULT
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(MDF). Within the scope of the invention hybrid molecules were produced which contain at least a portion of an early MDF and at least a portion of a late MDF covalently linked. The EPO sequence given is effective within the scope of the invention in full or in a truncated version. In: These compounds can be used to promote heamatopoiesis in a patient. The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDA co act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins egreen! Allows a molecular manner of the compounds are useful for treating anaemias of various origins egreen!
                                                                                                                                    61 VEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                64 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
                                                                           9
                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant haematopoietic molecules useful in treating anaemia(s) -comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIDS. It is easier to produce and administer one recombinant molecule rather than two separate molecules
                                     4 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                         1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
 Gaps
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0
                                                                                                                                                                                           PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                 121 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erythropoietin, EPO: erythrocytes; IL-3; haematopoiesis.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant hematopoietic molecule portion 2.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                           AAR23593 standard; protein; 166 AA
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
   166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1990;
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Human erythropoietin receptor agonist polypeptide - used to stimulate the production of red blood cells in a patient.
                             61 VEVWQGLALLSBAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                  VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
Erythropoietin receptor agonist; EPO; human; anaemia;
haematopoietic deficiency; red blood cell; erythroid progenitor;
                                           169
                                                      166
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                                                                                                                                                                                                                                                                                      Claim 1; Page 93; 112pp; English.
                                                                                                                                                                                                                                      Summers
                                                                                      AAW58404 standard; protein; 166
                                                                                                                                                                                                  97WO-US018703.
                                                                                                                                                                                                             96US-0034044P
                                                                                                             (first entry)
                                                                                                                                                                                                                         (SEAR ) SEARLE & CO G D.
                                                                                                                                                  bone marrow suppression.
                                                                                                                                                                                                                                      Mcwherter CA, Feng Y,
                                                                                                                          Human erythropoietin.
                                                                                                                                                                                                                                                   WPI; 1998-272221/24.
                                                                                                                                                                                                                                                         N-PSDB; AAV31031
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                  23-OCT-1997;
                                                                                                                                                                                                              25-OCT-1996;
                                                                                                                                                                          WO9818926-A1
                                                                                                             12-OCT-1998
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                                                                                                  AAW58404;
                    64
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                                                                                AAW58404
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Gaps

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Indels

Length 166;

Matches 166; Conservative

Query Match Best Local Similarity

97.9%; Score 851; DB 2; I 100.0%; Pred. No. 7.8e-86; ive 0; Mismatches 0;

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Misc-difference 41.
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                                                                      VEVWQGLALLSEAVLRQQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                N-terminus are optionally
                                                                                                                                                                                                                             Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO; human; chimeric protein; stem cell expansion; tumour; infection; autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
                                     4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                           Gaps
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Misc-difference 29. .30
Misc-difference 30. .30
Misc-difference 30. .31
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                                                                                                                                                                                                                                                                                                                                                          C- and N-termini"
                                                                                                                                                                                                                                                                                                                                                                                         new C- and N-termini"
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/note= "possible positions of new C- and N-termini"
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                                                                                                         169
                                                                                                                Length 166;
core 851; DB 2; Length 100 Pred, No. 7.88-86;
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                                                                                                       PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR
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/note= "1-6 amino acids of the
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/note= "possible positions of
32. .33
/note= "possible positions of
33. .34
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te= "possible positions of
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/note= "possible positions of
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            100.0%; Prec. .v..
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       97.9%; Score 851;
                                                                                                                                                                                                              Human EPO receptor agonist polypeptide
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                                                                                                                                                              AAW77780 standard; protein; 166
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                        Conservative
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                Similarity
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                       166;
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       Query Match
Best Local S
Matches 166
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Misc-difference 81. 85

Misc-difference 82. 83

Misc-difference 82. 83

Misc-difference 82. 83

Misc-difference 84. 85

Misc-difference 85. 86

Misc-difference 85. 86

Misc-difference 86. 87. 88

Misc-difference 87. 88

Misc-difference 86. 89

Misc-difference 87. 88

Misc-difference 80. 89

Misc-difference 108. 109 42. .43 [Note: "possible positions of new C- and N-termini" 43. .44 15. .46 /note= "possible positions of new C- and N-termini" 16. .47 Misc-difference 49. .50 /note= "possible positions of new C- and N-termini" /note= "possible positions of new C- and N-termini" Misc-difference 50. .51 N-termini" N-termini" and N-termini" C- and N-termini" and N-termini" C- and N-termini" and N-termini" and N-termini" C- and N-termini" N-termini" C- and N-termini" and N-termini" and N-termini" C- and N-termini" and N-termini" and N-termini" of new C- and N-termini" /note= "possible positions of new C- and N-termini" Misc-difference 117. .118 N-termini" of new C- and N-termini" 'note= "possible positions of new C- and and and and and ပ် /note= "possible positions of new C-44. .45 ပ် ပ် ပ် ပ် η ť /note= "possible positions of new C-112. .113 /note= "possible positions of new C-113. .114 of new C-ပ် force = "possible positions of new C/note = "possible positions of new Cnew new 'note= "possible positions of new 51. .52 /note= "possible positions of new 53..54 /note= "possible positions of new 'note= "possible positions of new positions of new "possible positions of new /note= "possible positions of new 111. .112 of new oĘ οĘ positions Misc-difference 47. 48
//note= "possible positions Misc-difference 48. .49 note= "possible positions note= "possible positions positions positions positions /note= "possible /note= "possible 52. .53 note= "possible" 14. .115 'note= "possible 15. .116 /note= "possible 116. .117 /note= "pr 110. .111 109. Misc-difference 45. Misc-difference 43. Misc-difference 46. Misc-difference 42. Misc-difference 44. Misc-difference Misc-difference

/note= "1-5 amino acids of the C-terminus are optionally /note= "possible positions of new C- and N-termini" 130...131note= "possible positions of new C- and N-termini"  $131.\ .132$ 122. .123 /note= "possible positions of new C- and N-termini" 123. .124 /note= "possible positions of new C- and N-termini" 125. .126 /note= "possible positions of new C- and N-termini" /note= "possible positions of new C- and N-termini" [29. ,130 'note≈ "possible positions of new C- and N-termini" note= "possible positions of new C- and N-termini" 'note= "possible positions of new C- and N-termini" 'note= "possible positions of new C- and N-termini" C- and N-termini" 'note= "possible positions of new C- and N-termini" 'note= "possible positions of new C- and N-termini" 'note= "possible positions of new C- and N-termini" note= "possible positions of new C- and N-termini" Staten NR; Feng Y, Mckearn JP, Summers NL, S Minnerly JC, Minster NI, Woulfe SL; 'note= "possible positions of new .26. .127 97WO-US020037. 96US-0029629P .128 .122 .129 .125 .166 .121 118. .119 (SEAR ) SEARLE & CO G D. WPI; 1998-261504/23. Misc-difference Mowherter CA, Streeter PR, 25-OCT-1996; WO9817810-A2 23-OCT-1997; 30-APR-1998

Multi-functional chimeric haematopoietic receptor agonist - useful to treat haematopoietic disorders, tumours, infections or autoimmune diseases.

Claim 1; Page 762; 841pp; English.

modified EPO amino acid sequence of the formula provided in AAW77780, in modified EPO amino acid sequence of the formula provided in AAW77780, in which the N-terminus is joined to the C-terminus directly or via a linker, the polypeptide having new C- and N-termin at one of the positions indicated. Novel claimed multi-functional chimeric positions indicated. Novel claimed multi-functional chimeric capture receptor agonists (see AAW77812-22) have the formula R1-L1 receptor agonists (see AAW77812-22) have the formula R1-L1 receptor agonist polypeptide (see AAW77782); (d) a modified human stem cell factor receptor agonist polypeptide (see AAW77782); (d) a modified human interleukin-3 polypeptide (see AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784); (f) modified human interleukin-3 polypeptide (see AAW77785); (d) a modified human interleukin-3 polypeptide (see AAW77784); (e) thush at least R1 or R2 is selected from (a), (b) or (c) as above. The cut that at least R1 or R2 is selected from (a), (b) or (c) as above. The multi-functional chimeric haematopoietic receptor agonist can be used to stimulate the production of haematopoietic cells in a patient, for the ex vivo expansion of haematopoietic cells in a patient, for the expansion of haematopoietic cells in the production of dendritic

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                                                                                                      123
                                                                                                                     61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes modified erythropoietin (EPO) genes and expression vectors comprising the genes. The present sequence represents a protein sequence from the present invention
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                                                                  1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKKMEVGQQA
                                                4 APPRLICUSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 166;
                                                                                                                                                         124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                          Length 166;
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                       Indels
                                                                                                                                                                                                                                                                                                                                  Modified erythropoietin related gene protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%; Score 851; DB 3; I
100.0%; Pred. No. 7.8e-86;
:ive 0; Mismatches 0;
Score 851; DB 2; I
Pred. No. 7.8e-86;
         100.0%; Prec. ... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 15pp; Korean.
                                                                                                                                                                                                                                                      ABB07030 standard; protein; 166
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                                                                                                                                                                                                                                                                                                                                                              Modified erythropoietin; EPO
 97.98;
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                          Matches 166; Conservative
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 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                          21-JUN-2002
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Gillies S;

Way JC,

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The present sequence is human erythropoietin (EPO) mature protein. EPO has improved biological activity and an extended serum half life greater than 20 hours. The present invention relates to modified EPO forms such as fusion proteins comprising a FC portion of an immunoglobulin (Ig) molecule and an EPO molecule (FC-EPO). The FC portion is fused covalently through its C-terminus directly or indirectly to the EPO molecule, and where the FC portion as well as EPO portion may be modified or mutated. The invention also relates to non-fused EPO molecules which have a pattern of cysteines or disulphide bonding which is distinct from human of animal EPO. Paramaceutical compositions containing EPO are useful in the treatment of EPO deficient diseases such as anaemia, renal failure, HIV infection, blood loss and chronic disease that can be treated with haematopoietic growth factor
             Human, erythropoietin, EPO, antianaemic, nephrotrophic, anti-HIV,
vaccine, haemostatic, immunoglobulin, Ig, EPO deficient disease, anaemia,
renal failure, Human Immunodeficiency Virus, HIV;
                                                                                                                                                                                                                                                                                                                                      Novel modified erythropoietin forms such as fusion proteins, comprising Fc portion of an immunoglobulin molecule and a target molecule having the biological activity of erythropoietin forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR
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                                                                                                                                                                                                                                                                    Sobel
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                                                                                                                                                                                                                                                                   Rieke
                                                         haematopoietic growth factor,
                                                                                                                                                                                                          99US-0164855P
                                                                                                                                                                                                                                     MERE ) MERCK PATENT GMBH
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                                                                                                                                                                                                                                                                                              WPI; 2001-367563/38
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Matches 166; Conserv
                                                                                                                                                                                                                                                                                                            N-PSDB; AAD06893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 166 AA;
                                                                                                                  WO200136489-A2
                                                                                                                                                                            03-NOV-2000;
                                                                                                                                                                                                          12-NOV-1999;
                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                    Hartmann A,
                                                                                                                                                25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to new conjugate having a modified erythropoietin glycoprotein, useful for stimulating red blood cell production, and for treating or preventing diseases correlated with anaemia in chronic renal failure, AIDS or cancer patients. The present sequence is a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                                                                       Erythropoietin glycoprotein; anaemia; chronic renal failure; AIDS;
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                                                                                                                            #2 relating to modified erythropoietin glycoprotein.
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Pred. No. 7.8e-86;
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                                     ABB83622 standard; protein; 166 AA.
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99US-0150225P.
99US-0151548P.
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                                                                                                                                                                                                                                 NO200003372-A.
                                                                                                                                                                                                   Unidentified.
                                                                                                                                                                                                                                                                                          28-JUN-2000;
                                                                                                                                                                                                                                                                                                                     02-JUL-1999;
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31-AUG-1999;
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      RESULT 14
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chronic renal failure; AIDS; cancer.

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The present invention relates to a conjugate comprising, human erythropoietin glycoprotein (EPO) having at least one free amino group and having in vivo biological activity of causing an increase the production of reticulocytes and red blood cells, covalently linked to 1-3 lower-alkoxy poly(ethylene glycol) groups through a linker. The invention is useful for preparation of medicaments for the treatment of prophylaxis of disease correlated with anemia in chronic renal failure patients (CRF), AIDS and for the treatment of cancer patients undergoing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 VEVWQGLALLSEAVLRÇQALLVNSSQPWEPLQLHYDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                    Novel erythropoietin-glycoprotein conjugate useful for treating diseases correlated with anemia in chronic renal failure patients, AIDS and for treating cancer, is linked to polyethylene glycol through linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%; Score 851; DB 4; Length 166; 100.0%; Pred. No. 7.8e-86; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                     (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Fig 2; 40pp; English
                                                                                                                                                                                   99US-0147452P.
99US-0151454P.
                                                                                                                                                                     99US-0142243P
                                                                                                                                    28-JUN-2000; 2000WO-EP006009
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Matches 166; Conservative
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                                                                  WO200102017-A2.
                                                                                                                                                                   02-JUL-1999;
05-AUG-1999;
30-AUG-1999;
                                   Homo sapiens.
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Search completed: November 19, 2004, 21:05:44 Job time : 59.4932 secs

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LENGTH: 166 amino acids TYPE: amino acid
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          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-883-795A-34
US-08-156B-34
US-09-55-265B-4
US-09-6(4-871-1
US-09-6(4-871-1
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US-09-55-265B-2
US-09-55-265B-2
US-09-55-265B-30
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                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB
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Sequence 70, Application US/08318193
Fatent No. 5641663
GENERAL INFORMATION:
APPLICANT: GARVIN, Robert T.
APPLICANT: GARVIN, Robert T.
TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
TITLE OF INVENTION: STIMULATIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
TITLE OF INVENTION: PROTEINS FACTOR (GN-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
                                   44,
49,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
US-09-552-265B-26
US-09-552-265B-31
US-09-552-265B-42
US-09-552-265B-18
US-09-552-265B-23
US-09-552-265B-34
US-09-552-265B-34
US-09-552-265B-34
US-09-552-265B-49
US-09-552-265B-37
US-09-552-265B-37
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                        US-09-552-265B-43
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
: USA
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97.9%; Score 851; DB 1; Length 166; 100.0%; Pred. No. 4.4e-98;

linear

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APPLICANT: Brigham and Women's Hospital
APPLICANT: 75 Francis Street
APPLICANT: Boston, MA 02115
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PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION WUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 166
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                    US-09-604-938-2
                                                                                                                                                        TYPE: PRT
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                                                                                                                                                             61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                                      64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                          1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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         0; Gaps
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    0; Indels
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Patent No. 6583272;
GENERAL INFORMATION:
APPLICANT: Ballon, Pascal
TILLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFREENCE: 1097 nomprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR FILING DATE: 1999-11-17;
PRIOR FILING DATE: 1999-108-13;
PRIOR APPLICATION NUMBER: 60/151,548
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Higger, Berne
APPLICANT: Higger, Berne
APPLICANT: JOSEI, Hans-Peter
TITLE REFERENCE: 1098 nonprovisional
CURRENT FILING NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 3
COFTWARE: PATENTING DATE: 1999-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.9%; Score 851; DB Best Local Similarity 100.0%; Pred. No. 4.4¢ Matches 166; Conservative 0; Mismatches
         0; Mismatches
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; Sequence 2, Application US/09604871
; Patent No. 6340742
      166; Conservative
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LENGTH: 166
TYPE: PRT
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                                                                                                               4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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| Sequence 2, Application US/09462941
| Patent No. 6608183
| GENERAL INFORMATION:
| APPLICANT: COX III, George N
| APPLICANT: Bolder Biotechnology, Inc.
| APPLICANT: Bolder Biotechnology, Inc.
| TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins FILE REFERENCE: 4152-1-PUS
| CURRENT APPLICATION NUMBER: US/09/462,941
| CURRENT FILING DATE: 2000-01-14
| PRIOR FILING DATE: 1997-07-14
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PatentIn Ver. 2.0
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97.9%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.4e-98;
Matches 166; Conservative 0; Mismatches 0; Indels
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97.9%; Score 851; DB 4; Length 166;
100.0%; Pred. No. 4.4e-98;
Live 0; Mismatches 0; Indels
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Batent No. 5322837

GENERAL INFORMATION:

APPLICANT: Hewick, Rodney M.

TITLE OF INVENTION: BEYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
APPLICANT: Bunn, H. Franklin
APPLICANT: Wen, Danyi
APPLICANT: Showers, Mark O.
TITLE OF INVENTION: Erythropoietin Muteins With Enhanced
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
ANDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                             COUNTEY. U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.9%; Score 851; DB 5; I
100.0%; Pred. No. 4.4e-98;
tive 0; Mismatches 0;
                                                                                                                  STREET: Sterne, Ressler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 21-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600 TELEPAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 166; Conservative
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COMPUTER READABLE FORM:
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TOPOLOGY: both
PCT-US94-04361-37
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: New York
RY: USA
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64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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US-08-883-795A-34

i Sequence 34, Application US/08883795A

i Sequence 34, Application US/08883795A

i Retent No. 5985607

i GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve

i TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
INVMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEB: BRRESXIN & PARR
STREET: 40 King Street West
CITY: Toronto
STRATE: Ontario
COUNTRY: Canada
ZIP: M5H 372

COMPUTER: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPUTER: IBM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19920731
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION UNMERR: 40,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 851; DB 1; I
Pred. No. 5.6e-98;
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97.9%; Score 851; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 166; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 1248/27
TELEPHONE: (202) 429-1776
TELEPHONE: (202) 429-1776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 193 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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Uemori, Takashi

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                                                                                                                                                                                                                                                                                                                                                                                                                                  88 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 147
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Sequence 4, Application US/09552265B
Patent No. 6555343
GENERAL INFORMATION:
APPLICANT: DeSauvage, Frederick
APPLICANT: Desauvage, Frederick
APPLICANT: Henner, Dennis, J.
TITLE OF INVENTION: No. 6555343e1 chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypeptides and nucleic acids encoding the same FILE REFERENCE: GENERY: 05776P1
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: US 09/307307
PRIOR FILING DATE: 1999-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 PPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
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100.0%; Pred. No. 5.6e-98;
iive 0; Mismatches 0;
                                                                                                                                                                                                                               Query Match
97.9%; Score 851; DB 2; I
Best Local Similarity 100.0%; Pred. No. 5.6e-98;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
TELECOMMUNICATION INFORMATION:
                   TELEPHONE: (416) 364-7311
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                TYPE: amino acide
TOPOLOGY: little
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 166; Conservative
                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-883-795A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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US-09-552-265B-4
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Sequence 34, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
RAPPLICANT: Asada, Kiyozo

RESULT 9 US-09-366-009-34

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                         TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 848; DB 4;
Pred. No. 4.4e-97;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-Aug-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/09,156
FILING DATE: «Unknown»
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
ATTORNEY AGENT: 1NFORMATION:
NAME: WASIEN, GEARAID:
REFERENCE/COCKET NUMBER: 19,763
REFERENCE/COCKET NUMBER: 977.6507P
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34
                        Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Ueno, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.6%;
Best Local Similarity 99.4%;
Matches 165; Conservative
Ueno, Takashi
                                                                                                                                                                                                                                                                                                         ZIP: 19102
COMPUTER READABLE FORM:
                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-809-156B-34
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64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.4%; Score 846; DB 4; Length 165; 100.0%; Pred. No. 1.8e-97; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           97.4%; Score 846; DB 3; I
100.0%; Pred. No. 1.8e-97;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09604938
Patent No. 6583272
GENERAL INFORMATION:
FAPFLICATURE BAILON, PASCAL
TITLE OF INVENTION:
FILE REPRENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/150,548
PRIOR FILING DATE: 1999-10-17
PRIOR APPLICATION NUMBER: 60/151,548
PRIOR FILING DATE: 1999-08-13
PRIOR PRIUNG DATE: 1999-08-13
PRIOR PRIUNG DATE: 1999-08-13
PRIOR PRIUNG DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 1
LENGTH: 165
    FILE REFERENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 200-06-28
FRIOR APPLICATION NUMBER: 60/151,454
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SECTAMARE: Patentin Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 165; Conservative
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Matches 165; Conservative
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-09-604-938-1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                        LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                             US-09-604-871-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.6%; Score 848; DB 4; Length 412;
99.4%; Pred. No. 4.4e-97;
tive 1; Mismatches 0; Indels
                   APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     ZIP: 19102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CURSSIFICATION: 435
                                                                                                                                                         ADDRESSEE: WELSER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09604871
Patent No. 6340742
GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: O'-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: J3-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: G8-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: Weiser, Gerard J.
REFERENCE/DOCKET NUMBER: J97.6507P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 215-875-8383
TELEFHONE: 215-875-8384
INFORMATION FOR SEQ ID NO: 34:
FUNCTION FOR SEQ ID NO: 34:
Koyama, No. 6472204uto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.4°
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-604-871-1
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124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 168

64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123

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US-09-552-265B-2
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                                                                                                                                                                                      APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Carcagno, Carlos Marcelo
APPLICANT: Melo, Carlos
APPLICANT: Welo, Carlos
TITLE OF INVENTION: Host Cells Expressing Recombinant Human Erythropoietin
FILE REFRENCE: 1909, 0020002
CURRENT APPLICATION NUMBER: US/09/830,967
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: AR 99-01-0679
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Sterrenbeld Biotechnologie No. 6777205th America, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.4%; Score 846; DB 4; Length 165; 100.0%; Pred. No. 1.8e-97;
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Anthony ATKINSON
TITLE OF INVENTION: Detection of Molecules in Samples
NUMBER OF SEQUENCES: 9
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ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/554,451
FILING DATE: 15-May-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred .v.
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Patent No. 6680207
GENERAL INFORMATION:
                                                                                                        Sequence 1, Application US/09830967
Patent No. 6777205
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ZIP: 20005
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.1
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-09-554-451-8
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                                                                                              US-09-830-967-1
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                    121
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Sequence 2, Application US/09552265B

Patent No. 655343

GENERAL INFORMATION:

TAPLICANT: Desauvage, Frederick

APPLICANT: Debauvage, Frederick

TITLE OF INVENTION: No. 655343el chimpanzee erythropoietin (chepo)

TITLE OF INVENTION: Dolypeptides and nucleic acids encoding the same FILE REFERENCE: GENERAL .05/09/552,265B

CURRENT APPLICATION NUMBER: US/09/552,265B

CURRENT PILING DATE: 2000-04-19

PRIOR APPLICATION NUMBER: US 09/307307

PRIOR APPLICATION NUMBER: US 09/307307

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 193
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Pred. No. 5.6e-97;
                                                                                                                                                                                                                                                                                                                                                             Query Match

97.0%; Score 843; DB 4; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.4e-97;
Matches 164; Conservative 1; Mismatches 0; Indels
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              FILING DATE: No. 6680207ember 16, 1998
APPLICATION NUMBER: GB 9723955.2
FILING DATE: No. 6680207ember 14, 1997
INFORMATION FOR SEQ ID NO: 88
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: PCT/GB98/03449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                    LENGTH: 165 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 99.4
Matches 165; Conservative
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ORGANISM: Pan troglodytes
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November 19, 2004, 21:11:10 ; Search time 80.087 Seconds (without alignments) 747.281 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/2/pubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Seguence 4. Appli		Rectained S	Segretary 2	Semience	Semience 2	Semience 2		Semience	'S SOUTH SOU	Parisa	Segrence	
SUMMARIES	ļ	ID	US-10-014-363-4	US-10-014-363-3	US-10-014-363-5	US-09-853-731-2	US-10-014-363-2	US-10-241-356-2	US-10-293-551-2	US-10-400-377-2	US-10-400-708-2	US-10-298-148-2	US-10-360-101-227	US-10-467-115-1	US-10-658-834A-201
		BB	13	13	13	6	13	14	14	14	14	14	15	15	16
	Query	Length	169	174	174	166	166	166	166	166	166	166	166	166	166
•₩	Query	Match	100.0	98.6	9.86	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9	97.9
	Ċ	score	869	856.5	856.5	851	851	851	851	851	851	851	851	851	851
	Result	NO.	н	~	m	4	Ŋ	9	7	80	σ	10	11	12	13

iequence sequence seq	888, 91, 63, 70, 81,
10-773-939-2 10-774-149-2 10-468-49-2 10-468-49-2 10-612-665-1 10-612-665-1 10-612-665-1 10-65-694-1 10-65-694-1 10-65-694-1 10-65-894-1	US-10-612-665-88 US-10-612-665-91 US-10-676-694-63 US-10-676-694-64 US-10-676-694-70 US-10-676-694-81
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1666 1093 1093 1093 1093 1066 1066 1093 1093 1093 1093	193 193 193 193
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11111112222222222244444444444444444444	0 4 4 4 4 0 11 6 4 4 4 0 11 6 4 6 6

ALIGNMENTS

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61 QQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKE 120
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                                                                                    APPLICANT: Bugel, Alfred
APPLICANT: Brance, Reinhard
APPLICANT: France, Reinhard
APPLICANT: France, Reinhard
APPLICANT: France, Bernd
APPLICANT: Tischer, Wilhelm
APPLICANT: Fischer, Wilhelm
APPLICANT: Fischer, Wilhelm
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT FILLING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
                    ; Sequence 4, Application US/10014363; Publication No. US20020115833A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: CHO/dhfr-
US-10-014-363-4
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JS-10-014-363-4
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                                                                                                     56 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 115
                                                                                                                                      61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
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                                        1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
          1 APP----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
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Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-00-863-731-2
Sequence 2, Application US/09853731
Sequence 2, Application US/09853731
Fatent No. US20020037841A1
GENERAL INFORMATION:
APPLICANT: Papadimitriou, Apollon
TITLE OF INVENTION: Erythropoietin Composition
FILE REFERENCE: 20619 US
CURRENT APPLICATION NUMBER: US/09/853,731
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: EP/00110355.5
NUMBER: OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10014363

Publication No. US20020115833A1

GENERAL INFORMATION:
APPLICANT: Burg. Josef
APPLICANT: Franze, Reinhard
APPLICANT: Franze, Reinhard
APPLICANT: Franze, Reinhard
APPLICANT: Tischer, Milhelm
APPLICANT: Tischer, Wilhelm
APPLICANT: Tescher, Wilhelm
APPLICANT: Tescher, Wilhelm
APPLICANT: Tescher, Wilhelm
APPLICANT: Townsynton: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
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ORGANISM: Homo sapiens
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US-09-853-731-2
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LENGTH: 166
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LENGTH: 166
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                           121 AISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
121 AISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 174;
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                                                                                                                                                  Sequence 3, Application US/10014363
; Publication No. US20020118833A1
; GRENERAL INFORMATION:
GAPPLICANT: Burg, Joseff
APPLICANT: Franze, Reinhard
APPLICANT: Franze, Reinhard
APPLICANT: Tranze, Martwut Ernst
APPLICANT: Tischer, Walhelm
APPLICANT: Tischer, Walhelm
APPLICANT: Tischer, Walhelm
APPLICANT: Genurg, Manfred
TITLE REFERENCE: Case 20805
FILE REFERENCE: Case 20805
CURRENT PILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
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Sequence 5, Application US/10014363

Publication No. US20020115833A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Engel, Alfred

APPLICANT: Franze, Reinhard

APPLICANT: Finger, Bernd

APPLICANT: Tischer, Wilhelm

APPLICANT: Worny, Manfred

TITLE REFERENCE: Case 20805

CURRENT APPLICATION NUMBER: US/10/014,363

CURRENT FILING DATE: 2001-12-11

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.1
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SEQ ID NO 3
LENGTH: 174
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Best Local Similarity 97.1
Matches 169; Conservative
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US-10-014-363-5
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ORGANISM: CHO/dhfr-
US-10-014-363-3
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TRNGTH: 174
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-10-014-363-3
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                                    97.9%; Score 851; DB 13; Length 166;
100.0%; Pred. No. 1.3e-84;
tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                    Length 166;
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Publication No. US20030077753A1
GENERAL INFORMATION:
I APPLICANT TISCHER, WILHELM
ITILE OF INVENTION: DIGLYCOSYLATED ERYTHROPOIETIN
FILE REPERENCE: 20971
CURRENT PILING DATE: 2002-09-11
PRIOR APPLICATION NUMBER: EP 01122555.4
PRIOR PILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 97.9%; Score 851; DB 14; Best Local Similarity 100.0%; Pred. No. 1.3e-84; Matches 166; Conservative 0; Mismatches 0;
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Fublication No. US2003012004541
GENERAL INCORMATION:
APPLICANT: Bailon, Pascal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/293,551
CURRENT FILING DATE: 2002-11-14
FRIOR PILING DATE: 2000-06-27
FRIOR PILING DATE: 1999-11-17
FRIOR APPLICATION NUMBER: 60/166,151
FRIOR FILING DATE: 1999-11-17
FRIOR FILING DATE: 1999-08-13
                                  Query Match
Best Local Similarity 100.
Matches 166; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 166
US-10-014-363-2
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j Education No. US20030162949A1

j GENERAL INFORMATION:
   APPLICANT: COX III, George

j FILE REFERENCE: 4152-1-PUS

j FILE REFERENCE: 4152-1-PUS

j CURRENT APPLICATION NUMBER: US/10/400,377

CURRENT FILING DATE: 2003-03-26

j PRIOR PILING DATE: 2000-01-14

j PRIOR PILING DATE: 2000-01-14

j PRIOR FILING DATE: 1997-07-14

j NUMBER OF SEQ ID NOS: 41

j SOFTWARE: PatentIn Ver. 2.0

j EQ ID NO 2

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97.9%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION WUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 166
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US-10-400-708-2
Sequence 2, Application US/10400708
Publication No. US20030166865A1
GENERAL INFORMATION:
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US-10-293-551-2
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SEQ ID NO 227
LENGTH: 166
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Squence 2, Application US/10298148

Publication No. US20330171284A1

GENERAL INPORMATION:

APPLICANT: Cox III, George N

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE REFERENCE: 4152-11-PUS

CURRENT APPLICATION NUMBER: US/10/298,148

CURRENT FILING DATE: 2000-11-15

PRIOR PLILING DATE: 2000-01-14

PRIOR PLILING DATE: 1997-01-14

PRIOR FILING DATE: 1997-07-14

NUMBER OF SEC ID NOS: 41

SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
ITILE BOLDER Biotechnology, Inc.
ITILE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 166
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97.9%; Score 851; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 166; Conservative
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US-10-298-148-2
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Sequence 227, Application US/10360101

Publication No. US20040009550A1

Sequence 227, Application US/10360101

GENERAL INFORMATION:
APPLICANT: Leenhouts, Cornelis J.
TITLE OF INVENTION: Export and modification of (poly) peptide in the lantibiotic way
FILE REPERENCE: 2183-5673

CURRENT APPLICATION NUMBER: US/10/360,101

CURRENT FILING DATE: 2003-02-07

PRIOR FILING DATE: 2002-05-24

NUMBER OF SEQ ID NOS: 309

SOFTWARE: Patentin version 3.1
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97.9%; Score 851; DB 15; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.3e-84;
Matches 166; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 166;
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Publication No. US20040063917A1

GENERAL INFORMATION:
APPLICANT: Carr, Gradam
APPLICANT: Carr, Gradam
APPLICANT: Jones, Tim
APPLICANT: Williams, Stephen
TITLE OF INVENTION: MODIFIED ERYTHROPOIETIN (EPO) WITH
TITLE OF INVENTION: REDUCED IMMUNOGENICITY
FILE REFERENCE: MER-114
CURRENT APPLICATION NUMBER: US/10/467,115
CURRENT APPLICATION NUMBER: 0102615.0
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.9%; Score 851; DB 15; Best Local Similarity 100.0%; Pred. No. 1.3e-84; Matches 166; Conservative 0; Mismatches 0;
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ORGANISM: Homo Sapien
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61 VEVWQGLALLSEAVLRGQALLVNSSQPWEFLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
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APPLICANT: Cox III, George N
APPLICANT: Cox III, George N
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
ITLE REFERENCE: 4152-1-PUS
CURRENT APPLICATION NUMBER: US/10/714,149
CURRENT PILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR PLING DATE: 2000-01-14
PRIOR PLING DATE: 1997-07-14
SPRIOR FILING DATE: 1997-07-14
SPRIOR FILING DATE: 2000-01-14
SPRIOR PLING DATE: 2000-01-14
SPRIOR FILING DATE: 2000-01-14
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100.0%; Pred. No. 1.3e-84;
iive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-84;
iive 0; Mismatches 0;
PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1907-07-14
NUMBER OF SEQ ID NOS: 41
SOFWARE: Patentin Ver: 2.0
SEQ ID NO 2
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Sequence 2, Application US/10774149

Publication No. US20040175800A1

; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 166; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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publication No. US20040132977A1

GENERAL INFORMATION:
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Guyon, Thierry
APPLICANT: Drittanti, Lila
APPLICANT: Manuel
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
TITLE OF INVENTION: Molecules and Related Applications
TITLE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A

CURRENT FILING DATE: 2003-09-08

PRIOR PLILING DATE: 2003-03-21
PRIOR PLILING DATE: 2003-03-21

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 1306

SCFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 201
                                                                                                                                                  61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
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APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REPERENCE: 415-21-PUS:
CURRENT APPLICATION NUMBER: US/10/773,939
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/10/400,377
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DATABASE ACCESSION NUMBER: Genbank AAA52400
DATABASE ENTRY DATE: 1994-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/10773939; Publication No. US20040175356Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Job time : 81.087 secs

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GenCore version 5.1.6
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                   Copyright
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OM protein - protein search, using sw model

Run on:

November 19, 2004, 20:59:24; Search time 19.6132 Seconds (without alignments) 829.068 Million cell updates/sec

US-10-014-363-4 Perfect score:

1 APPAPPRLICDSRVLERYLL......NFLRGKLKLYTGEACRIGDR 169 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	מסיים לידריריסמפט		erythropoietin pre	erythropoietin pre				ū			•	erythropojetin - d	ı	ū	megakarvocyte gro	ribonucleoside-din	Solute binding rec		probable 2-hydroxy		thrombopoietin pre	genome polyprotein	probable sensory	ATP-dependent heli	EGF receptor subst	transport	erved hypoth	methylamine utiliz	tropable conner-	hypothetical prote	hypothetical prote
SUMMARIES	qi		OHOZ	JQ0173	184613	m	2814	I46401	A24902	C769	146578	I46199	G02729	I80105	A55530	AB0323	AE0959	A83274	AI0443	856639	JC4125	GNWVJ8	T35681	AF0526	A54696	T35450	AG2919	H97693	S36741	AD1928	875569
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	Length		193	192	192	188	192	194	192	195	190	175	353	353	286	323	346	339	296	480	326	0	1829	813	897	348	455	455	747	242	451
ب	Query Match			89.1			81.2						11.2	11.0	10.7					9.6		٠		•	9.0					8.9	
	Score	1 1 1	425	7.14.5	769.5	718	206	690.5		685.5	683	638	76	96	93	88	87.5	85	83.5	83.5	81	80.5	79.5	78.5			78	78	78	77.5	
	Result No.	i	-	7	m	4	വ	9	7	<b>6</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

60 kD chaperonin [	d - Twos uiuoidwos	bacterioferitin x	mandelate racemase	thrombopoietin - m	groEL protein ~ Ba	hypothetical prote	conserved hypothet	rtS beta (AF305057	ATP-dependent heli	RF2 protein - saim	ribonucleoside-dip	chaperonin, 60 Kd	chaperonin 60 - Co	PSE1 protein - vea	dsu
B84932	B42281	HB2810	AE3465	\$45330	837039	S75772	AB2922	C97696	D64738	B37994	AH3625	B82048	S39765	853978	855517
2 B84932	2 B42281	2 HB2810	2 AE3465	2 \$45330	2 \$37039	2 875772	2 AB2922	2 C97696	2 D64738	2 B37994	2 AH3625	2 B82048	2 \$39765	2 S53978	2 \$55517
7	7	7	7	356 2 \$45330	7	7	400 2 AB2922	0	7	282 2 B37994	335 2 AH3625	544 2 B82048	552 2 839765	1089 2 853978	2
7	7	7	7	7	7	7	400 2	0	824 2 1	282 2	335 2	544 2	552 2	1089 2 8	1564 2 S
7	7	7	8.8 425 2	7	8.7 544 2	8.7 637 2	8.6 400 2	8.6 425 2	824 2 1	282 2	335 2	544 2	552 2	1089 2 8	1564 2 S

## ALIGNMENTS

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Cythropoietin precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 09-Jul-2004
C;Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 09-Jul-2004
C;Accession: A01855; A24744; A25384; A22210; S56178
R;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; See Nature 313, 806-810; 1985
A;Jitle: Isolation and characterization of genomic and cDNA clones of human erythropoiet A;Reference number: A01855; MuID:85137899; PMID:3838366
A;Accession: A01855
A;Molecule type: MRA; DNA
A;Residues: 1-193 «JAC»
A;Cross-references: UNIFROT:P01588; GB:X02157; GB:X02158
R;Lih, F.K.; Suggs, S.; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl Acad. Sci. U.S.A. 82, 7580-7584, 1985
A;Title: Cloning and expression of the human erythropoietin gene.
A;Reference number: A24744; MuID:8607948; PMID:3855178
A;Residues: 1-193 «LIN»
A;Residues: 1-193 «LIN»
A;Residues: 1-193 «LIN»
A;Residues: Communication of human erythropoietin.
A;Reference number: A25384; MUID:86140080; PMID:3949763
A;Accession: A25384

A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Rolecule type: 28-86,'Q',87-193 <LAI>
A,Experimental source: urine
A,Bxperimental source: urine
A,Note: forms without the carboxyl-terminal residue and the four carboxyl-terminal resid
R,Yanagawa, S.; Hirade, K.; Ohnota, H.; Sasaki, R.; Chiba, H.; Ueda, M.; Goto, M.
J. Biol. Chem. 259, 2707-2710, 1984
A,Title: Isolation of human erythropoietin with monoclonal antibodies.
A,Title: Lolation of human erythropoietin PhilD:6698989

A,Molecule type: protein A,Residues: 28-33,'X',35-37 <MTS> Coment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o C,Genetics: A;Accession: A22210
A;Molecule type: protein
A;Molecule type: 27 (X,131-33,11,13,11,13)
B;Molecule type: 27 (163-1172,1995
B;Molecule type: 27 (163-1172,1995
B;Molecule type: protein
A;Molecenice number: S56178; MUID:95284365; PMID:7766897

A,Cross-references: GDB:119110; OMIM:133170 A,Map position: 7q21.3-7q22.1 A,Introns: 5/1; 53/3; 82/3; 142/3

C; Function:

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R,Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A,Title: Exthropoietin structure-function relationships: High degree of sequence homolo
A,Reference number: 146083; WUID:93372347; PMID:8364201
                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q28513; GB:L10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C,Comment: Erythropoietin is produced by Kidney or liver of adult mammals and by liver o
C;Function:
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Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function relationships: High degree of sequence homold
A;Reference number: 146083; WUID:93372347; PMID:8364201
A;Accession: 146083
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C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of;
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 QAVEVWQGLALLSEAVLRGQAVLANSSQPFEPLQLHMDKAISGLRSITTLLRALGAQ-EA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 PGAPPRIVCDSRVLERYLLEAKEAENVTMGCSESCSLNENITVPDTKVNFYAWKRIEVGQ 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: 184613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erythropoietin precursor - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: 146083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 APPRLICDSRVLERYILEAREAENVTMGCAEGCSFSENITVPDTKVNFYTWKRMDVGQQA
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C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F;1-22/Domain: signal sequence (fragment) #status predicted <51G>
F;23-188/Product: erythropoietin #status predicted <MAT>
F;29-183,51-55/Disulfide bonds: #status predicted
F;46,60,105/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148/Binding site: carbohydrate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: erythropolesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-192/Product: erythropoletin #status predicted <WAT>
F;34-187,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Description: the primary inducer of erythrocyte formation C, Superfamily: erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 769.5; DB 1;
Pred. No. 1.5e-65;
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Pred. No. 1.1e-60;
                                                                                                                                                                                                                                             A,Accession: 184613
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 88.6%; al Similarity 89.9%; 151; Conservative
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ilarity 84.3%;
Conservative
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Matches
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C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human exprise member: JQ0173; MUD:87055236; PMID:2877922
A;Reference number: JQ0173; MUD:87055236; PMID:2877922
A;Residues: 1-192 <LIN>
A;Residues: 1-192 <LIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
       A,Description: the primary inducer of erythrocyte formation C;Superfamily: erythropoietin C;Keywords: erythropoietin C;Keywords: erythropoiesis; glycoprotein, hormone; kidney; liver F;1-27/Domain: signal sequence #status predicted <SIG> F;28-193/Product: erythropoietin #status experimental <MAT> F;34-188,56-66/Disulfide bonds: #status experimental <ARIS,5110/Binding site: carbohydrate (Asn) (covalent) #status experimental F;151,65,110/Binding site: Carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 APPRLICDSRVLERYLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 193
                                                                                                                                                                                                                                                                                                                   97.9%; Score 851; DB 1; Length 193, 100.0%; Pred. No. 2.8e-73;
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Pred. No. 5e-66;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. w..
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Best Local Similarity 100.
Matches 166; Conservative
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Best Local Similarity
Matches 153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 4-15,'L',17-107,'P',109-194 <WEN>
A;Cross-references: GB:L10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C;Function:
                                                     R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Exrthropoietin structure-function relationships: High degree of sequence homolc A;Reference number: 146083; MUID:93372347; PMID:8364201
A;Accession: 147077
                       Cross-references: UNIPROT: P33709; EMBL: Z24681; NID: 9395049; PIDN: CAA80848.1; PID: 93950
                                                                                                                                                                                                                                                                                                                                                                                                    */Journal of the primary inducer of erythrocyte formation C.Superfamily: erythropoietin C.Superfamily: erythropoietin C.Superfamily: erythropoietin C.Superfamily: erythropoietin C.Steywords: erythropoietin #status predicted cSIG. F.1-27/Domain: signal sequence #status predicted cSIG. F.1-81/Product: erythropoietin #status predicted cMAT> F.34-189, $56-60/Disulfide bonds: #status predicted F.51, $6.60/Disulfide: carbohydrate (Asn) (covalent) #status predicted F.51, $6.10/Binding site: carbohydrate (Ser) (covalent) #status predicted
A; Residues: 1-194 <FUX>
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Blood 62, 1507-1516;
Blood 62, 1507-1516, 1993
A,Title: Exthropoietin structure-function relationships: High degree of sequence homology. In 162748; MUID: 93372347; PMID:8364201
A,Reference number: 146083; MUID:93372347; PMID:8364201
A,Accession: 162748
A,Residues: translated from GB/EMBL/DDBJ
A,Residues: translated from GB/EMBL/DDBJ
A,Residues: GB-L192 - RES>
A,Cross-references: GB-L10608; NID:g204060; PIDN:AA41126.1; PID:g204061
C; Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of A,Pescription: the primary inducer of erythrocyte formation
C; Superfamily: erythropoietin
C; Superfamily: erythropoietin
C; Superfamily: erythropoietin
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                                                  64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: S28148; I62743
R;Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, Riodyys. Act 1171, 99-102, 1992
A;Title: Nucleotide sequence of rat erythropoietin.
A;Reference number: S28148; MUID:93042015; PMID:1420369
A;Accession: S28148
A;Molecule type: mRNA
A;Residues: 1-192 <NAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Keywords: erythropoissis; glycoprotein; hormone; kidney; liver
1.26/Domain: signal sequence #status predicted <SIG>
7.7-192/Product: erythropoietin #status predicted <MAT>
33-187,55-165/Disulfide bonds: #status predicted
50,64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
                                                                                                                                         124 PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
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Best Local Similarity 82.5*
Matches 137; Conservative
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A;Accession: A24901
A;Molecule type: DNA
A;Residues: 1-67, 'P', 69-192 <MCD>
A;Residues: 1-67, 'P', 69-192 <MCD>
A;Cross-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of C;Genetics:
C;Genetics:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: A24902
A, Molecule type: DNA
A, Molecule type: 1192 cSH0>
A, Cross-references: UNIPROT: P07321
A, Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 a
A, Note: the authors translated the codon TTA for residue 43 a
A, Note: the authors translated the codon TTA for residue 43 a
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A, Note: the authors translated the codon TTA for residue 
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                                                                                                                                                                                                                                                                                                              28 APPRLICDSRVLERYILEAREAENATMGCAEGCSFSENITVPDTKVNFYAWKRMEVQQQA
                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 LPDATPSAAPLRIFTVDALSKLFRIYSNFLRGKLTLYTGEACRRGDR
                                                                                                            Indels
     Score 690.5; DB 1;
Pred. No. 4.6e-58;
9; Mismatches 20;
          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythropoietin precursor - mouse C;Species: Mus musculus (house mouse)
     79.5%;
Query Match 79.5
Best Local Similarity 82.0
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਯ
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C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C.Accession: 146401; 147077
R.Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A.Title: The sheep erythropoletin gene: molecular cloning and effect of hemorrhage on paracession: 146401; MUID:93351736; PMID:8349021
A.Accession: 146401
A.Accession: Lanslated from GB/EMBL/DDBJ
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erythropoietin - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 146199
R;Wen, D; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Brythropoietin structure-function relationships: High degree of sequence homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-175 <WEN>
A;Residues: 1-175 <WEN>
A;Cross-references: UNIPROT:P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; PID:g55234<sup>7</sup>
C;Superfamily: erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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C.Species: Edmo sapiens (man)
C.Species: Edmo sapiens
C.Species: Edmo sapiens
C.Species: Edmo sapiens
C.Species: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C.Accession: G02729
R.Species: EMBL Data Library, May 1996
A.Reference number: H01637
A.Reference number: H01637
A.Recession: G02729
A.Recession: G02729
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Recessidues: 1.353 < IMX>
A.Cross-references: EMBL:U59493; NID:g1401245; PIDN:AAB03392.1; PID:g1401246
C.Genetics:
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                                                                                                                                                                                               23 APPRLICDSRVLERYILEAKEGENATMSCAESCSFSENITVPDTKVNFYAWKRMEVQQQA
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                                                                                                                                                    4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 LPDASPSSATPLRTFAVDTLCKLFRNYSNFLRGKLTLYTGBACRRRDR 190
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       Length 190;
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11.2%; Score 97; DB 2; Length 353;
Best Local Similarity 26.8%; Pred. No. 0.18;
Matches 42; Conservative 20; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 PPDA--ASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
   Score 683; DB 2;
Pred. No. 2.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: mRNA
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Query Match
78.6%; Score 683; DB
Best Local Similarity 82.1%; Pred. No. 2.3e
Matches 138; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 LPEEASPAPLRTFTVDTLCKLFRIYSNFLRGKL
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C;Accession: U7699
R;Vilalta, A.; Wu, D.; Margalith, M.; Hobart, P.
Biochem. Biophys. Res. Commun. 284, 823-827, 2001
A;Title: Rabbit EPO gene and cDNA: Expression of rabbit EPO after intramuscular injectic
A;Reference number: JC7699; WUID:21290682; PMID:11396976
A;Contents: Kidney
A;Accession: JC7699
A;Molecule type: DNA
A;Residues: 1-195 <VIL>A;Comment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
C;Gomment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
C;Gomment: This protein, a heavily glycosylated 34K protein growner: A;Gene: epo
C;Superfamily: erythropoietin
C;Keywords: glycoprotein; kidney
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Biood 82, 1507-1516, 193
Biood 82, 1507-1516, 193
A;Title: Exythropoietin structure-function relationships: High degree of sequence homology, A;Accession: 146083; MUID:93372347; PMID:8364201
A;Reference number: 146083; MUID:93372347; PMID:8364201
A;Accession: 146578
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A;Accident type: mRNA
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                                                                                                                                                                                                                                                                                                             64 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 APARLICDSRVIERYILEAKEAENVTWGCAEGCSLGENITVPDTKVNFHHWKKSEAGRHA 88
                                                                                                                                                                                                                                          86
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                          27 APPRLICDSRVLERYILBAKEAENVTMGCAEGPRLSENITVADTKVNFYAWKRMEVEEQA
                                                                                                                                                                    4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 PPDTTPPAPLRTLTVDTFCKLFRVYANFLRGKLKLYTGEVCRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
           Length 192;
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Pred. No. 1.4e-57;
           Query Match
78.9%; Score 686; DB 1;
Best Local Similarity 79.5%; Pred. No. 1.2e-57;
Matches 132; Conservative 14; Mismatches 20
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Best Local Similarity 81.4%;
Matches 136; Conservative 1
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C,Accession: A55530
R;Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkins, C.; Mar, V.; Suggs, S J. Biol. Chem. 270, 511-514, 1995
A;Title: Cloning and characterization of the human megakoryocyte growth and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Yersinia pest:
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: O2.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0323
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A55530; MUID:95122483; PMID:7822271
A;Accession: A55530
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Moss-references: GB:U17071
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             63 AVEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N,Alternate names: MPL ligand, long form
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSL----LGTO--
                                                                                                                                                                                                                                                                                                                                                         23 PAPP--ACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGEWKTQMEETK
                                                                                                                                                                                                                                                                                                3 PAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQ
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                                    A,Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 --LPPQG-----RTTAHKDPNAIFLSFQHLLRGKVR 161
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                                                                                                                                                                       11.0%; Score 96; DB 2; 26.8%; Pred. No. 0.22;
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             A; Cross-references: GDB:374007; OMIM:600044
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C,Keywords: alternative splicing; cytokine
                                                                                                                                                   Query Match
Best Local Similarity 26.8'
Watches 42; Conservative
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A55530
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A; Residues: 1-353 < RES>
A; Residues: 1-353 < RES>
A; Cross-references: UNIPROT: P40225; GB:L36051; NID:g533214; PIDN: AAC37568.1; PID:g533215
A; Accession: 180105
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-353 < RES>
A; Cross-references: GB:L36052; NID:g533216; PIDN: AAC37566.1; PID:g533217
B; de Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
Nature 369, 533-538
A; Title: Stimulation of megakaryocytopoiesis and throwbopoiesis by the c-Mpl ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Thrombopoietin precursor - human
NyAltante names: c-MPL ligand; megakaryocyte growth and development factor precursor
NyAltante names: c-MPL ligand; megakaryocyte growth and development factor precursor
C;Species: Homo sapiens (man)
C;Accesion: 159281; I80105; S$4531; S$48740; I38872; I52610
R;Accesion: 159281; I80105; S$4531; S$48740; I38872; I52610
R;Foster, D.C.; Sprecher, C.A.; Grant, F.J.; Kramer, J.M.; Kuijper, J.L.; Holly, R.D.; W
Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027, 1994
A;Title: Human hrombopoietin: gene structure, cDNA sequence, expression, and chromosoma
A;Accession: 159281; MUID:95108091; PMID:7809166
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A; Residues: 1-353 <SAU>
A; Cross-references: GB.133410; NID:9506826; PIDN:AAA59857.1; PID:9506827
B; Sohma, Y.; Akahori, H.; Seki, N.; Hori, T.; Ogami, K.; Kato, T.; Shimada, Y.; Kawamura
FEBS Lett. 353, 57-61, 1994
A; Title: Molecular cloning and chromosomal localization of the human thrombopoietin gene
A; Reference number: S48740; MUID:95010765; PMID:7926023
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A;Residues: 1-353 <SOH>
A;Residues: 1-353 <SOH>
A;COSS-references: GB:D32046; NID:g577319; PIDN:BAA06807.1; PID:g577320

R;BartLey, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.; Cell 77, 1117-1124, 1994

A;Title: Identification and cloning of a megakaryocyte growth and development factor tha A;Reference number: A54463; MUID:94291201; PMID:8020099

A;Accession: 138672

A;Status: preliminary
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A,Accession: 152610
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A;Accession: S45331
A;Status: preliminary
A;Wolecule run.
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A,Residues: 1-112, E'.114-353 <RE3>
A,Cross-references: EMBL:U11025; NID:g511223; PIDN:AAA50553.1; PID:g558078
K,Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
Blood 85, 981-988, 1995
                                                                                                                     63 AVEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKE 120
                                                                                                                                                                                     AQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSEQVRLLLGALQSL-----LGTQ-- 132
                                    PAPPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDIKVNFYAWKRMEVGQQ 62
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                                                                                                                                                                                                                                                                                             --LPPQG-----RTTAHKDPNAIFLSFQHLLRGKVR 161
                                                                                                                                                                                                                                                        121 AISPPDAASAAPLRIITADTFRKLFRVYSNFLRGKLK 157
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A;Residues: 1-353 <RE4>
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A, Status: preliminary
A, Molecule type: DNA
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Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar Solute binding receptor protein [imported] - Salmonella enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0959
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Retaus: preliminary
A;Retidues: 1-346 <PAR>
A;Crossion: AB0503
A;Residues: 1-346 <PAR>
A;Crossion: AB0503
A;Genetics: A
A;Status: preliminary
A;Molecule type: DNA
Cross-treferences: UNIPROT:Q8ZDC8; GB:AL590842; PIDN:CAC92889.1; PID:g15980631; GSPDB:G
C;Genetics:
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                                                                                69 GLALLSEAVLRGQALLVNSSQ-PWEPLQLHVDKAVSGLRSITTLLRALGAQ--KEAISPP 125
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No. 1.4; Matches 44; Conservative 22; Mismatches 48; Indels 5
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Best Local Similarity 25.2%; Pred. No. 1.1;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 19, 2004, 20:59:03; Search time 101.008 Seconds (without alignments) 962.682 Million cell updates/sec

US-10-014-363-4 869 1 APPAPPRLICDSRVLERYLL......NFLRGKLKLYTGEACRTGDR 169 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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33.2	# <u>15</u> 1	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

J.C., P.-H.,

AF202311; AR73133.1; JOINED. AF202311; AR7572.1; AF202314. AF202314; AAF23134.1; -.
AF202312; AAF23134.1; JOINED.
AF202313; AAF23134.1; JOINED.

S65458; AAD13964.1;

ZUHUZ

A01855;

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InterPro; IPR001913; 4 helix cytokine.
InterPro; IPR001913; EPO TPO.
InterPro; IPR001913; EPO TPO.
InterPro; IPR003013; EPO TPO.
InterPro; IPR003013; EPO TPO.
InterPro; IPR003013; EPO TPO.
INTERPO; IPR001915; EPO TPO.
IV.
PRIST; PR0017; EPO TPO; I.
PRINTS; PR00272; ERYHROPIN.
PROSITE; PS00817; EPO TPO; I.
SIGNCOLITE; PS00817; EPO TPO; I.
III STORMAR SIGNATION; GRANT SIGNAL III SIGNA
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EMBL, AF202308; AAF23132.1; --
EMBL, AF202306; AAF23132.1; --
EMBL, AF202306; AAF23132.1; JOINED.
EMBL, AF202310; AAF23133.1; --
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MEDITE=9844502? PubMed=9774108; DOI=10.1038/26773;

MEDITE=984502? PubMed=9774108; DOI=10.1038/26773;

A Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,

Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,

Burie J., Stroud R.M.;

Egrie J., Stroud R.M.;

Bricially or receptor orientation.";

Trificially or receptor orientation.";

I Nature 395:511-516(1998)

Tregulation of erythropoletin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

Tregulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

Tregulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

Tregulation of fetal or neonatal mammals.

TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals or the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex the names Epogen (Amgen), Epogin (Chugai), Epomax (Elanex), Eprex (Ortho Biocech). Variations in the glycosylation pattern of EPO distinguishes these products Epogen, Epogin, Eprex and Procrit or epoetin beta and Epomax as epoetin alfa, NeoRecormon and Recormon as epoetin beta and Epomax as epoetin of EPO (TPO family.

The SIMILARITY: Belongs to the EPO (TPO family.

The SIMILARITY: Belongs to the EPO (TPO family.

The SIMILARITY: MAME=RED Systems.com/asp?comerce book: EPO).

The SIMILARITY: Produced and pomax as epoetin alfa, NeoRecormon and Recormon and R
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Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Comparative study of the asparagine-linked sugar chains of human erythropoietins purified from urine and the culture medium of recombinant Chinese hamster ovary cells.";
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 28-57.
MEDLINE-84135751; PubMed-6698989;
Yanagawa S., Hirade K., Ohnota H., Sasaki R., Chiba H., Ueda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of human erythropoietin with monoclonal antibodies.";
J. Biol. Chem. 259:2707-2710(1984).
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MEDILE=29314463; PubMed=1820196;
Takeuchi M., Kobata A.;
"Structures and functional roles of the sugar chains of human
                                                TIŜSUBE-Urine;
MEDLINE=86144080; PubMed=3949763;
Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E.;
"Structural characterization of human erythropoietin.";
SEQUENCE OF 28-193, AND DISULFIDE BONDS
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                                                                                                                                                                                                        J. Biol. Chem. 261:3116-3121(1986)
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Erythropoietin.

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/FTIGHTWAR 009870.
P -> Q (in an hepatocellular carcinoma).
/FTIGHTWAR 009871.
E -> Q (in Ref. 1; CAA26095).
Q -> QQ (in Ref. 5).
G -> R (in Ref. 1; CAA26095).
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               Removed in mature form (Probable)
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N-linked (GLONAC. .).
/FTIG=CAR 000192.
O-linked (GalNAC. .).
SL -> NF (in an hepatocellular
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                                       N-linked (GlcNAc.
/FTId=CAR 000052.
N-linked GlcNAc.
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Best Local Similarity 100.
Matches 166; Conservative
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EMBL; X02158; CAA26095.1; -.

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La Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,

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La Lin R.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R.,

Ronkey erythropoietin gene: cloning, expression and comparison with

Un che human erythropoietin gene: ",

Gene 44:201-209(1986).

Le FUNCTION: Erythropoietin is the principal hormone involved in the

regulation of erythrocyte differentiation and the maintenance of a

physiological level of circulating erythrocyte mass.

Lessure Subcellular Location: Produced by kidney or liver of adult mammals

C - Subcellular Locatiff: Produced by kidney or liver of adult mammals

C - Alssyn Specificity: Produced by kidney or liver of adult mammals

C - SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopitheciae; Macaca
                                               01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
  192 AA.
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HSSP; P01588; ICN4.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001323; BPO TPO.
InterPro; IPR003013; Brythroptn.
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                                                                                                                            VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
              4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 63
                                               28 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.3e-71;
ive 0; Mismatches 0; Indels
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009488; AAP22357.1; -.
Hypothetical protein.
SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 AA.
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"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Matches 166; Conservative
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Submitted (MAY-2001)
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Brythropoletin.
By similarity.
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N-linked (GlCNAc.
N-linked (GlCNAc.)
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Matches 143; Conservative
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Name=EPO;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93372347; pubMed=8364201;
Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czeluaniak J., Goodman M., Bunn H.F.;
Czeluaniak J., Goodman M., Bunn H.F.;
Erythropoietin structure-function relationships: high degree of
sequence homology among mammals.";
Blood 82:157-1516(1993).
-: FUNCTION: Brythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
-: SUBCELLUAR LOCATION: Secreted.
-: TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
and by liver of fetal or neonatal mammals.
-: SIMILARITY: Belongs to the EPO / TPO family.
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Brythropoietin.
By similarity.
By similarity.
N-linked (GloNAc...) (N-linked (GloNAc...) (N-linked (GloNAc...) (O-linked (GalNAc...) (O-linked (GalNAc...) (O-linked (GalNAc...) (Colonked (GalNAc...) (Colo
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Pred. No. 5.5e-64;
9; Mismatches 7
                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque)
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                                                                                                                                                                                                                                        Erythropoietin precursor. Name=EPO;
                                                                                          STANDARD;
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192 AA;
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SEQUENCE
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KRMEVGOQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney;
PubMed=14719696;
Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
Kijima-Suda I.,
"Nucleotide sequence of equine erythropoietin and characterization of region-specific antibodies.";
Am. J. Vet. Res. 65:15-19(2004).
EMBL; AB100030; BAC55239.1; ...
HSSP; P01588; 1BJY.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Perissodactyla; Equidae; Equus.
NCBI TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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81.7%; Pred. No. 3.9e-60;
ive 10; Mismatches 15; Indels 7,
122 ISPPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR 169
                                                              145 ISLPDAASAAPLRTITADTFCKLFRVYSNFLRGKLKLYTGEACRRGDR 192
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Last annotation update)
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01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Erythropoietin precursor.
                  Name=Epo;
Rattus norvegicus (Rat).
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CARBOHYD
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                              FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

SUBCELDULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                            SEQUENCE OF 5-192 FROM N.A.
MEDLINE=93372347; PubMed=8354201;
MEDLINE=93372347; PubMed=8354201;
Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czelusniak J., Goodman M., Bunn H.F.,
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin.
By similarity.
By similarity.
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 711; DB 1; Length 192; 83.7%; Pred. No. 1.7e-58; tive 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
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EMBL; L10606, AAA30807.1; -.
FIR; 146083; 146083.
HSSP; P01588; 1BUY.
InterPro; IPR009079; 4 helix cytokine.
InterPro; IPR001313; EPO TPO.
InterPro; IPR001313; EPO TPO.
InterPro; IPR001313; EPO; 1.
PIRSF; PIRSF001951; EPO; 1.
PRINTS; PR00721; ERYTHROPTN.
PROSITE; PS00817; EPO; 1.
ERYTHROSYTE matration; Glycoprotein; Hormone; Signal.
SIGNAL
SIGNAL
SIGNAL
           Goodman R.E., Bell R.G.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
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61C5EA0F5E937293 CRC64;
                                                                                                                                                                                        and by liver of fetal or neonatal mammals. SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                       sequence homology among mammals.";
Blood 82:1507-1516(1993).
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20914 MW;
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Matches 139; Conservative
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192
187
59
50
64
109
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TISSUE=Kidney;
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EPO RAT STANDARD; PRT; 192 AA. P29576; P70694; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)

RESULT 7 EPO\_RAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goodman M., Bunn H.F.;
Goodman M., Bunn H.F.;
Goodman M., Bunn H.F.;
"Erythropoietin structure-function relationships: high degree of sequence homology among mammals.";
Blood 82:1507-1516(1993)
-! FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-! SUBCELBUIGHER LOCATION: Secreted.
-! TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-! SIMILARITY: Belongs to the EPO / TPO family.
Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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N-linked (GlcNAc. . ) (By similarity).
N-linked (GlcNAc. . ) (By similarity).
. . . . . . / GlCNAc. . ) (By similarity).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 4-192 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
Wen D., Boissel J.P.R., Tracy T.E., Mulcahy L.S., Czelusniak J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 192;
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                                                                                                                                                                                                            H., Ikura
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Thes 16; Indels
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                                                                                                             SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=93042015; PubMed=1420369;
Nagao M., Suga H., Okano M., Masuda S., Narita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.2%; Score 706; DB 1;
82.5%; Pred. No. 5e-58;
                                                                                                                                                                                                                                                              "Nucleotide sequence of rat erythropoietin.";
Biochim. Biophys. Acta 1171:99-102(1992).
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RGD; 2559; Epo.

InterPro; IPR009079; 4 helix cytt

InterPro; IPR001323; EPO TPO.

InterPro; IPR0030133; Erythroptn.
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PIRSF; PIRSF001951; BPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D10763; BAA01593.1; -. EMBL; L10608; AAA41126.1; -. PIR; S28148; S28148. HSSP; P01588; 1CN4.
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109
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109
192 AA;
                                                           NCBI_TaxID=10116;
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Erythropoietin precursor
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108
192 AA;
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05-JUL-2004
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CARBOHYD
SEQUENCE
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Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                      Canis familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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"Description of the full length of canine erythropoietin.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY572971; AA577874.1; -.
SEQUENCE 206 AA; 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 80.3%; Score 698; DB 2; Length 206; Best Local Similarity 81.3%; Pred. No. 3.1e-57; Matches 135; Conservative 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 LPEEASPAPLRTFTVDTLCKLFRIYSNFLRGKLTLYTGEACRRGDR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.3%; Score 698; DB 2; Length 206; 81.3%; Pred. No. 3.1e-57; ive 13; Mismatches 18; Indels
Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY572971; AS577874.1; -.
InterPro; IPR003079; 4 helix cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR003133; Erythroptn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00758; BPO_TPO; 1.
PRINTS; PR00272; ERTTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
SEQUENCE 206 AA, 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS77874;
15-APR-2004 (TrEMBLrel. 27, Created)
15-APR-2004 (TrEMBLrel. 27, Last sequence update)
15-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.3%
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                    Erythropoietin
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENTIAL SOURE-Kidney;

MINIALINE-96257233; PubMed-8666286;

A Suliman H.B., Majiwa P.A.O., Feldman B.F., Mertens B.,

Logan-Henfrey L.L.;

Logan-Henfrey L.L.;

Torining of a colbn benefing bovine erythropoietin and analysis of its

"Cloning of a colbn ending bovine erythropoietin and analysis of its

"Cloning of a colbn ending bovine erythropoietin and analysis of its

"Canactription in selected tissues.",

Gene 171:275-280(1996).

"Licentarion of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

"Tegulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

"TSUBCELLULAR LOCATION: Secreted.

"Insula SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.

"Insula SPECIFICITY: Perduced by Kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
41 APPRLICDSRVLERYILEAREAENVTMGCAQGCSFSENITVPDTKVNFYTWKRMDVGQQA 100
                                                                                                                               VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKBAIS 123
                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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By similarity.

N-linked (GLONAC. . .) (Potential).

N-linked (GLONAC. . .) (Potential).

N-linked (GLONAC. . .) (Potential).

DBC419022F7B483A CRC64;
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                                                                                                                                                                                                                                                                                                                                               161 LPEEASPAPLRTFTVDTLCKLFRIYSNFLRGKLTLYTGEACRRGDR 206
                                                                                                                                                                                                                                                                                                     124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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EMBL; U44762; AAB8653.1; -.
HSSP; P01588; 1CN4.
InterPro; IPR001932; 4 helix_cytokine.
InterPro; IPR001323; EPO_TPO.
InterPro; IPR001313; EPO_TPO.
InterPro; IPR001313; EPO_TPO.
PIRSF; PR05758; EPO_TPO; 1.
PIRSF; PR067751; EPO; 1.
PRNYS; PR067721; EPO; 1.
PRNYS; PR06772; EPO_TPO; 1.
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RESULT 12
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                                                    64 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                       85
                          26 APARLICDSRVLERYILEAREAENATMGCAEGCSFNENITVEDTKVNFYAWKRMEVQQQA
                 4 APPRLICUSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=87039105; PubMed=3773894;
Shoemaker C.B., Mitsock L.D.;
"Murine erythropoietin gene: cloning, expression, and human gene
   1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ICFW;
MEDLINE-98030528; PubMed-9365246;
Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
                                                                                       124 PPDAA-SAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                   MEDLINE=87039104; PubMed=3022133; McDonald J.D., Lin F.-K., Goldwasser B., "Cloning, sequencing, and evolutionary analysis of the mouse errthropoietin gene.", Mol. Cell. Biol. 6:842-848(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                Cheung T.L., Hardy L.C., Cheung T.L., Koop B.F.; "Comparative analysis of the gene-dense ACHE/TFR2 region chromosome 7q22 with the orthologous region on mouse chro Nucleic Acids Res. 29:1352-1365(2001)
  19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv;
MEDLINE=21138439; PubMed=11239002;
Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Bori Cheung T.L., Hardy_D.M., Schwartz S., Scherer S.W., Tsui
                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Mismatches
                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                              Cell. Biol. 6:849-858(1986),
 .
8
Matches 139; Conservative
                                                                                                                                                                                                 Erythropoietin precursor.
                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                       EPO MOUSE
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                                                                                                                                     RESULT 11
EPO MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93351736, PubMed=8349021,
Fu P., Evans B., Lim G.B., Moritz K., Wintour M.E.,
"The sheep erythropoietin gene: molecular cloning and effect of
hemorrhage on plasma erythropoietin and renal/liver messenger RNA in
                                                                                                                                                                                                                                                                                                                                                                                         By similarity.

N-linked (GLONAc. .) (By similarity).

N-linked (GLONAc. .) (By similarity).

N-linked (GLONAc. .) (By similarity).

65F94E214E0DEF2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Indels
                                                                                                                                                                                                     InterPro; 187009079; 4 helix_cytokine.
InterPro; IPR001323; EPO_TPO.
InterPro; IPR001313; EPO_TPO.
InterPro; IPR001313; EPO_TPO.
Pfam; PF00758; EPO_TPO; 1.
PRSF; PRSF001951; EPO_TPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 694; DB 1;
Pred. No. 6.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPO SHEEP STANDARD; PRT; 194 AA. 193709; Q28872; 01-FBB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adult sheep.";
Mol. Cell. Endocrinol. 93:107-116(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21365 MW;
                                                                                    EMBL; M12482; AAA37568.1; -.
EMBL; M12930; AAA37570.1; -.
EMBL; AF312033; AAK28825.1; -
EMBL; X11971; CAA72707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.9%;
80.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythropoietin precursor.
                                                                                                                                                                                                                                                                                                                                                                      192
187
50
64
109
                                                                                                                                                                                              MGD; MGI:95407; Epo.
                                                                                                                                                           PIR; A24902; A24902
HSSP; P01588; 1CN4.
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64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 APPRLICUSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.9%; Score 685.5; DB 2; Length 195; Best Local Similarity 81.4%; Pred. No. 4.3e-56; Matches 136; Conservative 12; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Wilalta A.1. Wu D. Margalith M., Hobart P.;

"Rabbit EPO gene and cDNA: expression of rabbit EPO after
intramuscular injection of pDNA.";

Biochem. Blophys. Res. Commun. 284:823-827(2001).

R Biochem. Blophys. Res. Commun. 284:823-827(2001).

R BABL; AF290943; AAG36961.1; -..

R HSSP; PO1588; ICN4.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0005128; F:erythropotetin receptor binding; IEA.

R GO; GO:0005128; F:erythropotetin receptor binding; IEA.

R GO; GO:0005128; F:erythropotetin receptor binding; IEA.

R InterPro; IPR001323; EPO TPO.

R InterPro; IPR00133; EPO TPO.

R Pfam; PF00758; EPO TPO; 1.

R PRINKS; PR00221; EPO TPO; 1.

R PRINKS; PR00221; EPO TPO; 1.

R PROSITE; PS00212; EPO TPO; 1.

R PROSITE; PS00212; EPO TPO; 1.

R PROSITE; PS00212; EPO TPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO, GO:0005276; C:extracellular; IEA.
CO, GO:0005128; F:erythropoietin receptor binding; IEA.
CO; GO:0005179; F:hormone activity; IEA.
CO; GO:0005179; F:hormone activity; IEA.
CINTERPRO; IPR001023; EPO TPO.
CINTERPRO; IPR001023; EPO TPO.
CINTERPRO; EPO TPO; 1.
CINTERPRO; PROFOSE; EPO TPO; 1.
CINTERPRO; PROFOSE; EPO TPO; 1.
CINTERPRO; PROSOZI; ERYTHROPIN.
CINTERPOSITE; PROBOZI; EPO TPO; 1.
CINTERPOSITE; PROBOZI; PRO
SEQUENCE FROM N.A.

Wilstan A., Wu D., Margalith M., Hobart P.;

Vilalta A., Wu D., Margalith M., Hobart P.;

Rabbit BPO gene and cDNA: expression of rabbit EPO after intramuscular injection of pDNA.";

Biochem. Biophys. Res. Commun. 284:823-827(2001).

EMBL; AF290944; AG36962.1;

HSSP; P01588; ICN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21290682; PubMed=11396976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.9%;
81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 APPRLICDSRVIERYILEAREAENATMGCAEGCSFSENITVPDTKVNFYAWKRMEVQQQA 87
                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.

Erythropoietin.
By similarity.
By similarity.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
F -> L (in Ref. 2).
L -> P (in Ref. 2).
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Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                          "Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%; Score 690.5; DB 1; Length 194; 82.0%; Pred. No. 1.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 LPDATPSAAPLRIFTVDALSKLFRIYSNFLRGKUTLYTGEACRRGDR 194
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9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C025AAB0528131A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; TRR009079; 4 helix cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001313; EPO TPO.
InterPro; IPR001313; Erythroptn.
Pfam; PF00758; EPO TPO; 1.
PIRSF; PIRSF001951; EPO; 1.
PRINTG; PR00817; EPO TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
               Goodman M., Bunn H.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                          Blood 82:1507-1516(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L10610; AAA31518.1; -. PIR; 146401. HSSP; P01588; ICN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z24681; CAA80848.1; -.
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Best Local Similarity 82.0
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
189
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110
16
108
194 AA;
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DISULFID
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CARBOHYD
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CONFLICT
SEQUENCE
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CHAIN

RESULT 13

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MEDIANE-3337247; PubMed=8364201;
MA Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
A Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
A Czelusniak J., Godman M., Bunn H.F.;
TEYAhropoietin structure-function relationships: high degree of
Sequence homology among mammals.",
Blood 82:1507-1516 (1993)
C -1- FUNCTION: Erythropoietin is the principal hormone involved in the
regulation of erythrocyte differentiation and the maintenance of a
physiological level of circulating erythrocyte mass.
C -1- SUBCELLULAR LOCATION: Secreted.
C -1- SUBCELLULAR LOCATION: Secreted by kidney or liver of adult mammals
C -1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals
C -1- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                           VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
                                                                                                             63
                                                                     88
                                              APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
(Potential).
(Potential).
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                                                                                                                                                        124 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001323; EPO TPO.
InterPro; IPR0013013; EPVHroptn.
PRIMTS; PR00272; ERVIHROPTN.
PROSTIE; PR00272; ERVIHROPTN.
IPROSTIE; PR00817; EPO TPO; 1.
InterProcyte maturation; Glycoprotein; Hormone; Signal.
NON_TER
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By similarity.
By similarity.
N-linked (GloNAc. .) (
N-linked (GloNAc. .) (
N-linked (GloNAc. .) (
N-linked (GloNAc. .) (
                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Erythropoietin precursor (Fragment).
   12; Mismatches
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                                                                                                                                                                                                                                                                        PRT;
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190 EX
190 BY
55 BY
46 N-
105 N-
168 N-
20888 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L10607; AAA31029.1; -. PIR; 146578; 146578.
HSSP; P01588; 1CN4.
136; Conservative
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig)
                                                                                            64
                                                                                                                                                                                       149
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Name=EPO
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CARBOHYD
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Matches
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EPO_PIG
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64 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 123
                                                                                                                      63
                                                                                     82
                                                                      4 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKEMEVGQQA
                                      Gaps
                                     7
                                                                                                                                                      124 PPDA--ASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 169
                                                                                                                                                                     143 LPDASPSSATPLRTFAVDTLCKLFRNYSNFLRGKLTLYTGEACRRRDR 190
              Length 190;
                                     21; Indels
          Score 683; DB 1;
Pred. No. 7.1e-56;
78.6%; Scor. 82.1%; Pred. No. /... 7; Mismatches
      Query Match
Best Local Similarity 82.1
Matches 138; Conservative
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Search completed: November 19, 2004, 21:10:59 Job time : 102.008 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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November 19, 2004, 20:57:38 ; Search time 61.2534 Seconds (without alignments) 1019.028 Million cell updates/sec Run on:

US-10-014-363-5 898 Perfect score:

1 APPGAAHYAPPRLICDSRVL......NFLRGKLKLYTGEACRTGDR 174 Sequence:

Scoring table:

2002273 seqs, 358729299 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB s Maximum DB s

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 233ep04:\*

1: geneseqp1980s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2001s:\*

6: geneseqp2003s:\*

7: geneseqp2003bs:\*

8: geneseqp2003ss:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ABB77900	ABB77898	ABB77901	ADJ71846	ABB77899	ABB77902	AAW99360	AAR71251	ADF15091	AAP70398	AAR23593	AAW58404	AAW77780	ABB07030	ABB83622	AAE02641	AAB66698	ABG92101	AAM53062	ABB77897	ADG65661	ABR39996	ABR57500	ADF70839	
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Length	174	174	201	205	169	196	376	167	769	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	
% Query Match	100.0	95.9	95.9	95.4	n l	45.4	7.00	4.0	4.	4.	94.8	4.		94.8	94.8	4	4	94.8	4.	4.	94.8	4.	•	94.8	
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ADL92150	ADK70564	ADL88867	ADL06781	AD059416	AAP50299	AAP50298	AAP60599	AAP81195	AAPS0300	ANDERES	7000000	AAF / 0256	AAR65499	AAR71137	AAR74141	AAR81982	44098397	10000000	AAY43398	AAY94530	AAY93638
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166	166	166	166	166	167	167	188	188	193	193	100	177	193	193	193	193	193	1 6	133	193	193
94.8	94.8	94.8	94.8		94.8	94.8	94.8	94.8	94.8	94.8	0. P.O	٠				94.8	94.8		74.0	94.8	94.8
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56	27	28	29	30	31	32	33	34	35	36	3.7		n i	ب ص	40	41	42	43	ř .	44	45

## ALIGNMENTS

Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor. Amino acid sequence of a modified human erythropoietin (EPO). ¥ ABB77900 standard; protein; 174 (first entry) 07-OCT-2002 ABB77900; RESULT 1 ABB77900 

Homo sapiens. Synthetic

1. .8 /note= "proteolytic cleavage site" 9. .174 /note= "BPO protein" Location/Qualifiers Cleavage-site Protein

WO200249673-A2

27-JUN-2002

20-DEC-2000; 2000EP-00127891.

08-DEC-2001; 2001WO-EP014434.

(HOFF ) HOFFMANN LA ROCHE & CO AG F.

Tischer Schurig HE, Engel A, Franze R, Hilger B, Burg J, Wozny M;

3

WPI; 2002-566640/60.

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

Disclosure; Page 39-40; 40pp; English.

The present sequence represents a modified human erythropoietin (EPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The

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specification describes a conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its analogues (where hEPO) is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycopylation sites covalently linked to a polycosylation site) and proposed is a rearrangement of a glycosylation site. The glycoprotein is covalently linked to a polycopylation site of production of reticulocytes and red blood cells. The EPO glycoprotein correased circulation of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma readidence time, decreased clearance, compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired circulating the division and differentiation of committed erythroid stimulating the division and differentiation of committed erythroid programments in the bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, erythropoietin, BPO, glycoprotein, reticulocyte production, red blood cell production, anaemia, chronic renal failure, acquired immunodeficiency syndrome, AIDS, cancer, bone marrow; committed erythroid progenitor.
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/note= "secretion signal peptide"
                                                                                                                                                                                                                                                                                                                      Score 898; DB 5;
Pred. No. 1.5e-89;
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                                                                                                                                                                                                                                                                                                        100.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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/note= "EPO protein"
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Matches 174; Conservative
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                                                                                                                                                                                                                                                                                           Sequence 174 AA;
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The present sequence represents a modified human erythropoietin (BPD)

Cr protein. The EPD was extended at the N-terminal by a proteolytic cleavage

Site. It was used to produce conjugates of the invention. The

Specification describes a conjugate comprising an EPD glycoprotein having

an N-terminal alpha-amino group, chosen from human EPO (hEPD) or its

an N-terminal alpha-amino group, chosen from human EPO glycoprotein having

cr a rearrangement of a glycosylation site). The glycoprotein is

cr a rearrangement of a glycosylation site). The glycoprotein is

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently linked to a poly(ethylene glycol) group. The EPO glycoprotein

crowlently alpha-amin planema residence time, decreased clearance,

increased clinical activity in vivo, improved potency and stability, when

crompared to unmodified EPO. The EPO conjugate is useful for preparing

crompared to unmodified EPO. The EPO conjugate is useful for preparing

compared to unmodified EPO. The EPO conjugate is useful for preparing

commandeficiency syndrome (AIDS) and for treating cancer patients

cundergoing chemotherapy. It is also useful for treating patients by

stimmlating the division and differentiation of committed erythroid

crowpared to the pone marrow
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                                                                                               conjugate of erythropoietin glycoprotein with polyethylene glycol, I for treating diseases correlated with anemia in chronic renal
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                                                                                                                                        failure patients and acquired immunodeficiency syndrome
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/note= "proteolytic cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 898; DB 5;
100.0%; Pred. No. 1.9e-89;
ive 0; Mismatches 0;
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Matches 174; Conservative
                                         WPI; 2002-566640/60.
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                                                               N-PSDB; ABL59291
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                                                                                                                                 useful for
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Wozny M;
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protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The SPO site. It was used to produce conjugate comprising an EPO site. It was used to produce conjugate comprising an EPO site. It was used to shall be amino group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein contains that and plasma residence time, decreased clarance, increased clinical activity in vivo, improved potency and stability, when compared to unmodified EPO. The EPO conjugate is useful for preparing compared to unmodified EPO. The EPO conjugate is useful for preparing anaemia in chronic renal failure parients (REP), acquired immunodeficiency syndrome (AIDS) and for treating cancer patients with consorting chemotherapy. It is also useful for treating patients by consorting patients in the hours manned.

"The EPO security of the comparing committed erythroid conversion in the hours manned."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents a modified human erythropoietin (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 38-39; 40pp; English.
                                                                                                                                                                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                  08-DEC-2001; 2001WO-EP014434
                                                                                                                                                                  20-DEC-2000; 2000EP-00127891
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                                                                                                                                                                                                                                                                   Engel A,
                        WO200249673-A2
                                                                     27-JUN-2002
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                                                                                                                                                                                                                                                                Burg J,
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Sequence 174 AA;

RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120 120 9 9 1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK 1 APPRIEGRAPPRLICDSRVLERYLLEAKRAENITTGCAEHCSLNENITVDDTKVNFYAWK 61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL Gaps 121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174 .; 0 tch 95.9%; Score 861; DB 5; Length 174; al Similarity 97.1%; Pred. No. 1.7e-85; Indels 169; Conservative 0; Mismatches 5; Indels Query Match Best Local Similarity 61 Matches g à Db δ g

Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; Amino acid sequence of a modified human erythropoietin (EPO) ABB77901 standard; protein; 201 AA 07-OCT-2002 (first entry) RESULT 4
ABB77901
XX
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AC ABB7
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DT 07-C
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acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; 28. .35 /note= "proteolytic cleavage site" /note= "secretion signal peptide" /note= "EPO protein" Location/Qualifiers committed erythroid progenitor. 36. .201 Cleavage-site Homo sapiens Synthetic Protein Peptide 

WO200249673-A2

Tischer W;

Schurig HE,

Franze R, Hilger B,

124

27-JUN-2002

08-DEC-2001; 2001WO-EP014434

20-DEC-2000; 2000EP-00127891.

(HOFF ) HOFFMANN LA ROCHE & CO AG F.

Schurig HE, Tischer W; Hilger B, Engel A, Franze R, Burg J, Wozny M;

WPI; 2002-566640/60.

N-PSDB; ABL59289.

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal fallure patients and acquired immunodeficiency syndrome.

Disclosure, Fig 3; 40pp; English.

profess. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugate comprising an EPO glycoprotein having an N-terminal alpha-amino group, chosen from human EPO (hepO) or its an alogues (where hEPO is modified by addition of 1-6 glycosylation sites) or a rearrangement of a glycosylation site). The glycosylation sites or a rearrangement of a glycosylation site). The glycosylation sites or a rearrangement of a glycosylation site). The glycosylation sites or a rearrangement of a glycosylation site). The glycosylation sites or a rearrangement of a glycosylation site). The EPO glycoprotein is covalently linked to a poly(ethylene glycol) group. The EPO glycoprotein conforted or teticulorytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance.

Compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRF), acquired anaemia in chronic renal failure patients (CRF), acquired cundergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow The present sequence represents a modified human erythropoietin (EPO)

Sequence 201 AA;

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                                                                                                                                                            61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
                                                                              1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                    28 APPRIEGRAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                                                                                                       88 RMEVGÓGÁVEVWÓGLÁLLSEAVLRGÓALLVNSSÓPWEPLGLHVDKAVSGLRSLTTLLRAL
                                              Gaps
                                                                                                                                                                                                                                             121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
                                                                                                                                                                                                                                                                                 148 GAQXEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
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0
      Length 201;
  Score 861; DB 5; Length 20:
Pred. No. 2.1e-85;
0; Mismatches 5; Indels
  tch 95.9%;
al Similarity 97.1%;
169; Conservative (
Query Match
                       Local
                                      Matches
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ABB77899 standard; protein; 169 AA.

RESULT 6 ABB77899 ABB77899;

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The invention comprises the amino acid and coding sequences of non-glycosylated erythropoietin (EPO) analogues, where the lysine at position 45 and/or 116 has been replaced with an amino acid that cannot be perylated. The non-glycosylated EPO analogues of the invention are useful for treating anaemia. The present amino acid sequence represents a non-glycosylated EPO analogue with a modified protease B signal peptide. NOTE: The present sequence is included in the sequence listing as SEQ ID No 29, however another sequence on page 28 of the specification is also shown as SEQ ID No 29.
                                                                                                                                                                                                                                                               Non-glycosylated EPO analogue with modified protease B signal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A non-glycosylated erythropoietin (RPO) analog useful treating anemia where the lysine at position 45 and/or 116 has been replaced with an amino acid that cannot be pegylated.
                                                                                                                                                                                                                                                                                                                               non-glycosylated erythropoietin analogue; EPO analogue; PEG; anaemia;
protease B signal peptide.
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/note= "Non-glycosylated EPO analogue region"
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Pred. No. 5.8e-85;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 29; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stewart DIH;
                                                                   ADJ71846 standard; protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003; 2003WO-CA001020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2002; 2002US-0396750P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 97.1
Matches 169; Conservative
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malek LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CANG-) CANGENE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-214326/20.
N-PSDB; ADJ71845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004009627-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
Unidentified.
                                                                                                                                                                                                   06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cossar JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
                     ADJUNE AND THE MENT OF THE MEN
RESULT
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The present sequence represents a modified human erythropoietin (EPO)

protein. The EPO was extended at the N-terminal by a proteolytic cleavage
site. It was used to produce conjugates of the invention. The
specification describes a conjugate comprising an EPO glycoprotein having
an N-terminal alpha-amino group, chosen from human EPO (hEPO) or its
analogues (where hEPO is modified by addition of 1-6 glycosylation sites
or a rearrangement of a glycosylation site). The glycoprotein is
covalently linked to a poly(cthylen glycol) group. The EPO glycoprotein
covalently linked to a poly(cthylen glycol) group. The EPO glycoprotein is
covalently linked to a poly(cthylen glycol) group. The EPO glycoprotein of
covalently linked activity of causing bone marrow cells to increase
circulating half-life and plasma readidence time, decreased clearance,
increased clinical activity in vivo, improved potency and stability, when
compared to unmodified EPO. The EPO conjugate is useful for preparing
compared to unmodified EPO. The EPO conjugate is useful for preparing
compared to the treatment and prophylaxis of diseases correlated with
compared to manodificate patients (CRF), acquired
anaemia in chronic renal failure patients (CRF), acquired
immunodeficiency syndrome (AIDS) and for treating patients by
cundergoing chemotherapy. It is also useful for treating patients by
stimulating the division and differentiation of committed erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.
                                                                                                                                       Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tischer W;
                                                                                              Amino acid sequence of a modified human erythropoietin (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schurig HE,
                                                                                                                                                                                                                                                                                                                                        1. .3
/note= "proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engel A, Franze R, Hilger B,
                                                                                                                                                                                                                                                                                                                                                                      4. .174 /
/note= "EPO protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 39; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulating the division and di
progenitors in the bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2001; 2001WO-EP014434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-2000; 2000EP-00127891.
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-566640/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200249673-A2
                                                                                                                                                                                                                                                                                                                                 Cleavage-site
                                                            07-OCT-2002
                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-2002
                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burg J,
Wozny M;
                                                                                                                                                                                                                                                                                                                                                                          Protein
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Gaps

5

Indels

95.4%; Score 856.5; DB 5; 97.1%; Pred. No. 5e-85; iive 0; Mismatches 0;

Query Match
Best Local Similarity 97.1
Matches 169; Conservative

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92 121

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GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174

61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL

32 AVPTPAAAAPPRLICDSRVLERYLLEAKBAENITTGCAEHCSLNENITVPDTKVNFYAWK APPGAAHYAPPRLICDSRVLERYLLBAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK

Length 169;

compared to unmodified EPO. The EPO conjugate is useful for preparing medicaments for the treatment and prophylaxis of diseases correlated with anaemia in chronic renal failure patients (CRP), acquired in immunodeficiency syndrome (AIDS) and for treating cancer patients undergoing chemotherapy. It is also useful for treating patients by stimulating the division and differentiation of committed erythroid progenitors in the bone marrow

Length 196;

5.

Score 856.5; DB 5 Pred. No. 6.2e-85;

95.4%; 97.1%;

Sest Local Similarity

Query Match

Sequence 196 AA;

88866666666

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RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
                                         |||-----APPRLICDSRVLERYLLEAKEAENITTGCAEHCSINENITVPDTKVNFYAWK 55
1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK 60
                                                                        GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                      Human; erythropoietin; EPO; glycoprotein; reticulocyte production; red blood cell production; anaemia; chronic renal failure; acquired immunodeficiency syndrome; AIDS; cancer; bone marrow; committed erythroid progenitor.
                                                                                                                                                                      Amino acid sequence of a modified human erythropoietin (EPO)
                                                                                                                                                                                                                                                                              28. .30 /note= "proteolytic cleavage site"
                                                                                                                                                                                                                                                                      /note= "secretion signal peptide"
                                                                                                                                                                                                                                                                                                        /note= "EPO protein"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                       ABB77902 standard; protein; 196 AA
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                              31. .196
                                                                                                                                                                                                                                                                                                                      WO200249673-A2
                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                        Homo sapiens,
                                                                                                                                                       07-0CT-2002
                                                                                                                                                                                                                                                                                                                                      27-JUN-2002
                                                                                                                                                                                                                               Synthetic
                                                                121
                                                                                                                                       ABB77902:
                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                              Protein
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61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120
                                                                                                                                                                                                                                                                                                                                                                                          Human, erythropoietin, dimer, trimer, polymer, fusion protein, cancer,
biological activity, anaemia, proliferation, differentiation, progenitor,
leucocyte, granulocyte, blood, myelosuppressed patient.
                                        9
                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein with increased activity comprising at least two protein molecules - used to, e.g. treat erythropoietin related deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein. The invention relates to the production of dimeric, trimeric or polymeric fusion proteins with increased biological activity. The fusion proteins are used to treat or prevent protein-related deficiency states, specifically, where the protein is erythropoietin (EPO; AAX25689), anaemia, but also for increasing proliferation, differentiation and activity of haematopoietic progenitors (e.g. increasing numbers of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents a human erythropoietin (EPO) homodimeric fusion
                                1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                              APP----APPRLICDSRVLERYLLEAKBAENITTGCAEHCSLNENITVPDTKVNFYAWK
                                                                                                                          83 RMEVGQQAVBVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL
                                                                                                                                                     121 GAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                          5
        Indels
    .0
                                                                                                                                                                                                                                                                                                                                                             Human erythropoietin homodimer fusion protein.
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 16A-C; 119pp; English.
                                                                                                                                                                                                                                                                        Ą
                                                                                                                                                                                                                                                                     AAW99360 standard; protein; 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       states for treatment of anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-00890929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00018138
                                                                                                                                                                                                                                                                                                                                (first entry)
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-120911/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX25701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sytkowski AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9902710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1998;
                                                                                                                                                                                                                                                                                                                                21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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The present sequence represents a modified human erythropoietin (BPO) protein. The EPO was extended at the N-terminal by a proteolytic cleavage site. It was used to produce conjugates of the invention. The specification describes a conjugate comprising an BPO glycoprotein having an N-terminal alpha-amin of group, chosen from human EPO (hEPO) or its analogues (where hEPO is modified by addition of 1-6 glycosylation sites or a rearrangement of a glycosylation site). The glycoprotein is covalently linked to a polly(ethylene glycol) group. The EPO glycoprotein bas in vivo biological activity of causing bone marrow cells to increase production of reticulocytes and red blood cells. The conjugate increased circulating half-life and plasma residence time, decreased clearance, increased clinical activity in vivo, improved potency and stability, when

Novel conjugate of erythropoietin glycoprotein with polyethylene glycol, useful for treating diseases correlated with anemia in chronic renal failure patients and acquired immunodeficiency syndrome.

Disclosure, Fig 4; 40pp; English.

Tischer W;

Schurig HE,

Engel A, Franze R, Hilger B,

Burg J, Wozny M;

2002-566640/60. N-PSDB; ABL59290

(HOFF ) HOFFMANN LA ROCHE & CO AG F.

08-DEC-2001; 2001WO-EP014434. 20-DEC-2000; 2000EP-00127891, 0

Gaps

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Length 167; Indels

09 67

Matches

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σ RESULT

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61 AVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLSSLTTLRALGAQKEAI 120
                                                                                                                                                68 AVEVWOGLALLSEAVIRGOALLVNSSOPWEPLOLHVDKAVSGIRSLTTLLRALGAQKEAI 127
                                                                                                            1 YAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQ
                                                                            YAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           albumin fusion protein; albumin activity; human serum albumin; serum osmotic pressure; shelf-life; stability; antidiabetic; gene therapy; diabetes mellitus; human.
                                                                                                                                                                                                                       128 SPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                            Human albumin therapeutic fusion protein SeqID387
       Score 852; DB 2;
Pred. No. 1.5e-84;
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN GENOME SCI INC.
DELTA BIOTECHNOLOGY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-2002; 2002US-0370227P.

10-MAY-2002; 2002US-0370227P.

24-MAY-2002; 2002US-038950P.

28-MAY-2002; 2002US-038123P.

05-JUN-2002; 2002US-038123P.

10-JUL-2002; 2002US-0384625P.

24-JUL-2002; 2002US-0398008P.

09-AUG-2002; 2002US-0402131P.

13-AUG-2002; 2002US-0402131P.

18-SEP-2002; 2002US-041355P.
                                                                                                                                                                                                                                                                                                                                                       ADF15091 standard; protein; 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2001; 2001US-0341811P.
24-JAN-2002; 2002US-0350358P.
28-JAN-2002; 2002US-0351360P.
28-FEB-2002; 2002US-035970P.
28-FEB-2002; 2002US-0360000P.
27-MAR-2002; 2002US-0367500P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0417611P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0420246P
         94.9%;
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                                              Matches 166; Conservative
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003060071-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                           ADF15091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
           Query Match
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                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                        ADF15091
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                                                                                                                    임
                                                                                                                                                         ਨੋ
                                                                                                                                                                                         셤
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                                                                                                                                                                                               265
                                                                                                                                                                                                                                 64 VGQQAVEVWQGLALLSEAVIRGQALLIVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 123
                                                                                                                                                                                                                                                      266 VGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQ 325
                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human erythropoietin; glycosylation; sialic acid; solubility; half-life; biological activity; proteolysis resistance; anaemia; chronic renal failure; analogue Ser103; O-linked carbohydrate chain.
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erythropoietin (EPO) analogues having additional glycosylation site(s) to increase sialic acid content, thereby increasing solubility, serum half-life, biological activity and resistance to proteclysis.
                                                                                                                                                                                           206 GGGSTAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRME
leucocytes and granulocytes in the blood of myelosuppressed patients) for treating cancer and other cell growth disorders
                                                                                                                                                           4 GAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRME
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                         KEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                           ..
                                                                                          Length 376;
                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "O-linked glycosylation site"
                                                                                    / Match 95.1%; Score 854; DB 2; Local Similarity 97.7%; Pred. No. 2.9e-84; hes 167; Conservative 0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human erythropoietin analogue Ser103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR71251 standard; protein; 167 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 5; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-00108016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US009257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Byrne TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-098764/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMGE-) AMGEN INC.
                                                        Sequence 376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9505465-A1
                    for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elliott SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR71251;
                                                                                                                                                                                                                                                                                                            124
                                                                                            Query Match
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New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
                                            MA
                                              Haseltine
                                              Rosen CA,
              PRINCIPIA PHARM CORP
                                               Turner AJ,
                                                                             WPI; 2003-598517/56.
                                               Ballance DJ,
(DELZ )
(PRIN-)
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Sequence 167 AA;

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This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may callow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating calbumin fusion protein is useful for preparing a composition for treating convel full-length human albumin therapeutic fusion protein of the convention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpot_sequences
                           Example 4; SEQ ID NO 387; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 769 AA;
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67 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA 126 78 QAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDRAVSGLRSLTTLLRALGAQKEA 137 7 HYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQ 18 HSAPPRLICDSRVLERYLLEAKBAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQ ö 127 ISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 173 Length 769; 1; Indels Score 852; DB 7; Pred. No. 1.3e-83; 0; Mismatches 94.9%; Matches 166; Conservative Best Local Similarity Query Match g ò qq à à

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77

AAP70398 standard; protein; 166 19-FEB-1991 AAP70398; 

(first entry)

Sequence of human erythropoietin (EPO).

Mega-karyocyte-platelet growth factor; hormone; mega-karyocyte colony stimulating factor; therapy; small acetyl cholinesterase positive cell; erythrocyte growth effect.

Ношо

JP62149624-A.

03-JUL-1987.

86JP-00191542 15-AUG-1986;

85JP-00203049. 13-SEP-1985;

(KAWA/) KAWAKITA M.

WPI; 1987-224837/32

Megakaryocyte-platelet growth factor - contains as active component human erythropoietin and is used to treat diseases caused by decrease in platelets.

Disclosure, Page 181; 8pp; Japanese.

All of the Cys residues in the SQ are labelled "SH". Megakaryocyte-platelet growth factor contains human BPO as an active principle. Human

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EPO has a megakaryocyte colony-stimulating activity and increases the ratio of small acetyl cholinesterase positive cell (SAchB+) which is immature megakaryocyte. Human EPO effects megakaryocyte-platelet system other than an erythxocyte growth effect. Megakaryocyte-platelet growth is usable as a remedy for diseases caused by a platelet decrease
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100.0%; Pred. No. 1.9e-84;
ive 0; Mismatches 0;
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AAR23593 standard; protein; 166 20-OCT-1992 AAR23593;

AA.

Erythropoietin; EPO: erythrocytes; IL-3; haematopoiesis. Recombinant hematopoietic molecule portion 2. Homo sapiens WO9206116-A, 

PHARM CORP (ORTH ) ORTHO

90US-00589958. 91WO-US007053

26-SEP-1991; 28-SEP-1990;

Rosen JI;

WPI; 1992-150819/18.

Recombinant haematopoietic molecules useful in treating anaemia(s) -comprise IL3 or GM-CSF and EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity

Disclosure; Page 32; 82pp; English.

This protein sequence given comprises the entire amino acid sequence of human erythropoletin (BPO). EPO leads to the maturation of erythrocytes and is therefore designated as a late myeloid differentiation factor (MDF). Within the scope of the invention hybrid molecules were produced which contain at least a portion of an early MDF and at least a portion of an early MDF and at least a portion of an early MDF and at least a portion of an early MDF and at least a portion of an early MDF equally linked. The EPO sequence given is effective within the scope of the invention in full or in a truncated version.

Anino acids 7-161 act as a late MDF when recombined with an early MDF eq. IL-3. These compounds can be used to promote heamatopolesis in a patient. The Epoding of the early and late factors allows a very high conc. of late MDF with early MDA to act more specifically to stimulate only the allows the early MDA to act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins eg.renal failure and

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AIDS. It is easier to produce and administer one recombinant molecule
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                                                                            Score 851; DB 2; I
Pred. No. 1.9e-84;
                                                                    94.8%; bcc. 100.0%; Pred. No. ... 0; Mismatches
                   rather than two separate molecules
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AAW58404 standard; protein; 166 AA 12-0CT-1998 AAW58404; AAW58404

Human erythropoietin. 

Erythropoietin receptor agonist; EPO; human; anaemia; haematopoietic deficiency; red blood cell; erythroid progenitor; bone marrow suppression.

Homo sapiens WO9818926-A1

07-MAY-1998

97WO-US018703 23-OCT-1997;

96US-0034044P 25-OCT-1996;

(SEAR ) SEARLE & CO G D.

ż Summers Feng Mcwherter CA,

WPI; 1998-272221/24. N-PSDB; AAV31031.

Human erythropoietin receptor agonist polypeptide - used to stimulate production of red blood cells in a patient.

Claim 1; Page 93; 112pp; English.

comprises a modified BPO amino acid sequence given in AAM58404, where (a) comprises a modified BPO amino acid sequence given in AAM58404, where (a) optionally 1-6 amino acids from the N-terminus and 1-5 from the C-terminus corp be deleted, (b) the N-terminus is joined to the C-terminus corporation and any two consecutive amino acids (c) there are new C- and N-terminia at any two consecutive amino acids from amino acids 23-24 to 38-39, 40-41 to 41-42, 43-44 to 48-49, 50-51 to 57-8; 77-78 to 82-83, 84-85 to 88-89, and 108-20 to 131-132, and (d) optionally the agonist polypeptide is preceded by Met, Ala, or Met-Ala. 60 Of these circularly permuted BPO receptor agonists (see AAW38413-72) are claimed. Also claimed are: nucleic acid molecules (see AAW30971-V31030) encoding novel BPO receptor agonists; a method of producing an BPO receptor agonist using transfected host cells, and methods for stimulating the production of transfected host cells, and methods for stimulating the production of haematopoietic cells, are selective ex vivo expansion of erythroid

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                                                                                                                                                                                                                                                                                         genitors, and treating patients having a haematopoletic disorder using BPO receptor agonists. The BPO recentor anniat activity agonists.
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                       the EPO receptor agonists. The EPO receptor agonists retain one or more activities of native EPO and may also show improved haematopoietic cellstimulating activity and/or an improved activity profile which may include reduction of undesirable biological activities associated with native EPO and/or have improved physical properties such as increased solubility, stability and refold efficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haematopoietic receptor agonist; erythropoietin receptor agonist; EPO; human; chimeric protein; stem cell expansion; tumour; infection; autoimmune disease; haematopoietic disorder; therapy; dendritic cell.
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/note= "possible positions of new C- and N-termini"
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WO9817810-A2 23-OCT-1997; 25-0CT-1996; Streeter PR, 30-APR-1998 diseases and N-termini" C- and N-termini" C- and N-termini" and N-termini" 42. .43 /note= "possible positions of new C- and N-termini" /note= "possible positions of new C- and N-termini" 14. .45 /note= "possible positions of new C- and N-termini" new C- and N-termini" N-termini" 47. .48 /note= "possible positions of new C- and N-termini" and N-termini" and N-termini" C- and N-termini" and N-termini" and N-termini" C- and N-termini" N-termini" C- and N-termini" N-termini" C- and N-termini" N-termini" and N-termini" and N-termini" new C- and N-termini" new C- and N-termini" and N-termini" new C- and N-termini" and C- and and and and C- and and and and ŋ ပ် new C-ပ် ပ် of new Cnew C-ပ new C-ပ ပ ပ် new Cnew Cnew Cnew Cnew new of new of new positions of new new /note= "possible positions of new 'note= "possible positions of new 'note= "possible positions of new 'note= "possible positions" of new 'note= "possible possible possible possible positions" of new 'note= "possible possible p new note= "possible positions of new new new new positions of new of new new new new new new /note= "possible positions of new T11...112 "possible positions of new 112...113 of oŧ /note= "possible positions of /note= "possible positions of 49. .50 /note= "possible positions of 50. .51 positions of oţ /note= "possible positions of 78..79 /note= "possible positions of 79. 80 /note= "possible positions of 85. .86 positions of positions of note= "possible positions of 'note= "possible positions of 11. .82 "possible positions of σŧ οĘ oŧ oŧ of of οĘ positions positions positions positions positions positions 'note= "possible positions 56. .57 'note= "possible positions 16. 87 'note= "possible positions 'note= "possible positions "possible positions "possible positions positions note= "possible positions positions "possible .38 Misc-difference Misc-difference

/note= "1-5 amino acids of the C-terminus are optionally deleted" and N-termini" C- and N-termini" and N-termini" 'note= "possible positions of new C- and N-termini"  $(62,\ .166$ and N-termini" and N-termini" and N-termini" and N-termini" and N-termini" and N-termini" N-termini" N-termini" N-termini" C- and N-termini" C- and N-termini" and and and and and and C- and C- and ڻ ن ڻ ပ် ပ် new C-ပ် ပ် new Cb ე ပ new C-ပ် ζ new new 'note= "possible positions of new nev new new new /note= "possible positions of new 127. 128 /note= "possible positions of new Misc-difference 128. .129 /note= "possible positions of new Misc-difference 129. .130 of new /note= "possible positions of new 125. .126 'note= "possible positions of new 30. .131 of new note= "possible positions of new /note= "possible positions of new 131, .132 Misc-difference 119. 120

Misc-difference 120. 121

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97WO-US020037

96US-0029629P.

(SEAR ) SEARLE & CO G D.

Staten NR; Feng Y, Mckearn JP, Summers NL, S' Minnerly JC, Minster NI, Woulfe SL; Mcwherter CA,

WPI; 1998-261504/23.

10 Multi-functional chimeric haematopoietic receptor agonist - useful treat haematopoietic disorders, tumours, infections or autoimmune

Claim 1; Page 762; 841pp; English.

A human erythropoietin (EPO) receptor agonist polypeptide comprises a modified EPO amino acid sequence of the formula provided in AAW77780, in which the N-terminus is joined to the C-terminus directly or via a linker, the polypeptide having new C- and N-termini at one of the positions indicated. Novel claimed multi-functional chimeric hamanachopietic receptor agonists (see AAW77812-22) have the formula R1-L1-R2, R2-L1-R1, R1-R2 or R2-R1, where L is a linker and R1 and R2 are independently selected from: (a) the human EPO receptor agonist; (b) a human stem cell factor receptor agonist polypeptide (see AAW77781); (c) a

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us-10-014-363-5.rag

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            human granulocyte colony stimulating factor (G-CSF) polypeptide (see AAW77783); (e) modified human interleukin-3 polypeptide (see AAW77784); (f) modified human interleukin-3 polypeptide (see AAW77784); (f) modified human c-mpl ligand polypeptide (see AAW77785); and (g) a factor selected from the group consisting of a CSF, a cytokine, a lymphokine, an interleukin and a haematopoietic growth factor, provided that at least R1 or R2 is selected from (a), (b) or (c) as above. The multi-functional chimeric haematopoietic receptor agonist can be used to stimulate the production of haematopoietic cells in a patient, for the ex vivo expansion of haematopoietic cells in a patient, for the expansion of haematopoietic cells in a patient.
                                                                                                                                                                                                                                                                                                                     69 VEVWOGIALLSEAVIRGOALLVNSSOPWEPLOLHVDKAVSGIRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                    61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes and represents
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human flt-3 receptor agonist polypeptide (see AAW77782); (d) a modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes modified erythropoietin (BPO) expression vectors comprising the genes. The present sequence a protein sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MODIFIED ERYTHROPOIETIN GENE AND EXPRESSION VECTORS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                          PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                   Length 166;
                                                                                                                                                                                                                      Indels
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100.0%; Pred. No. 1.9e-84;
iive 0; Mismatches 0;
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Matches 166, Conservative
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N-PSDB; ABL50878.
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                                                                                                                                                                                          Query Match
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-84;
Matches 166; Conservative 0; Mismatches 0;

Sequence 166 AA;

Length 166;

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9 APPRLICDSRVLERYLLBAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA

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69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                     1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                          174
                                                                          PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR
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Job time : 62.2534 secs
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Sequence Sequence Sequence

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Sequence 4 Sequence 1 Sequence 2 Sequence Sequence

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database

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Sequence 70, Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:
TENDEL INFORMATION:
TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS: 91
CORRESPONDENCE ADDRESS: 91
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: USA

STATE: Virginia
COMPUTER READABLE FORM:
MEDIUM TYPE: PRO COMPUTER PRODUCTS
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 851; DB 1; I
Pred. No. 1.7e-98;
  US-09-552-265B-26
US-09-552-265B-31
US-09-552-265B-42
US-09-552-265B-18
US-09-552-265B-23
US-09-552-265B-23
US-09-552-265B-33
US-09-552-265B-34
US-09-552-265B-49
US-09-552-265B-49
US-09-552-265B-21
US-09-552-265B-31
US-09-552-265B-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
APPLICATION NUMBER: US 07/224,568
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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Best Local Similarity
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Sequence 2, Appli
Sequence 37, Appl
Sequence 1, Appli
                                                                                                                                                                    (without alignments)
646.913 Million cell updates/sec
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                                                                                                                                        November 19, 2004, 21:00:09; Search time 17.8375 Seconds
                                                                                                                                                                                                                                                         898
1 APPGAAHYAPPRLICDSRVL.....NFLRGKLKLYIGEACRIGDR 174
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Sequence 45,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ABCTUS.COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-604-871-2
US-09-604-938-2
US-09-604-938-2
US-09-604-04361-37
US-08-883-795A-34
US-08-883-795A-34
US-08-883-795A-34
US-08-809-156B-34
US-09-604-871-1
US-09-604-871-1
US-09-604-871-1
US-09-604-871-1
US-09-655-265B-2
US-09-552-265B-2
US-09-552-265B-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COX III, George N
APPLICANT: COX III, George N
APPLICANT: Bolder Biotechnology, Inc.
ITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 415-21-FUS
CURRENT APPLICATION NUMBER: US/09/462,941
CURRENT FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
SOFTWARE: FEQ ID NOS: 41
SOFTWARE: PATCHIN Ver: 2.0
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94.8%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels
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94.8%; Score 851; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-98;
Matches 166; Conservative 0; Mismatches 0; Indels
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PCT-U594-04361-37
Sequence 37, Application PC/TUS9404361
Sequence 37, Application PC/TUS9404361
SEDERAL INFORMATION:
APPLICANT: Brigham and Women's Hospital
APPLICANT: Francis Street
APPLICANT: Boston, MA 02115
                      60/142,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09462941; Patent No. 6608183; GENERAL INFORMATION:
PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION UNMBER: 60/1
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                                                                                                               LENGTH: 166
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                                                                                                                                                 69 VEVWOGLALLSEAVLRGOALLVNSSOPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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Patent No. 6583272;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal
TITILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/604,938;
CURRENT FILING DATE: 2000-06-27;
PRIOR APPLICATION NUMBER: 60/166,151;
PRIOR FILING DATE: 1999-11-17;
PRIOR FILING DATE: 1999-08-13;
PRIOR FILING DATE: 1999-08-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ENTHHODIETIN CONJUGATES
FILE REPRENCE: 1098 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,871
CURRENT FILING DATE: 2000-66-28
PRIOR RILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              US-09-604-871-2; Sequence 2, Application US/09604871; Sequence 2, Application US/09604871; Patent No. 6340742; PERREAL INFORMATION: APPLICANT: Burg, Josef
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               166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-604-871-2
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Best Local Similarity
Matches 166; Conserv
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SEQ ID NO 2
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US-09-604-938-2
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               Matches
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TOPOLOGY:
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Patent No. 5322837
GENERAL INFORMATION:
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF
TITLE OF INVENTION: ERYTHROPOIETIN AND ERYTHROPOIETIN COMPOSITION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul H. Heller
STREET: Kenyon & Kenyon, One Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 851; DB 5; Length 166;
Pred. No. 1.7e-98;
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TITLE OF INVENTION: Erythropoietin Muteins With Enhanced TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04361
FILING DATE: Herewith
CLASSIFCATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/049,802
FILING DATE: 1-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0627.336PC01
TELECOMMUNICATION INFORMATION:
THE PROPERTY OF THE PRO
                                                                                                                                                                      STREET: 1100 New York Avenue, Suite 600 CITY: Mashington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

94.8%; Score 034, 22

Best Local Similarity 100.0%; Pred. No. 1.7

Matches 166; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Bunn, H. Franklin
Wen, Danyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acids
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COMPUTER READABLE FORM:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , TOPOLOGY: both
PCT-US94-04361-37
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US-07-903-220-1
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69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: AMANG, Gregor
APPLICANT: AWANG, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
TIPLE MEN NAME AND STATES
TO STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.8%; Score 851; DB 1; Length 193; Best Local Similarity 100.0%; Pred. No. 2.2e-98; Matches 166; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,220
FILING DATE: 19220731
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 1248/27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0796
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
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CLASSIFICATION: 435
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NAME: Gravelle, Michelline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-08-893-795A-34
Sequence 34, Application US/08883795A
; Patent No. 5985607
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              : 193 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Query Match
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                                                                                                                                                                                                                                                                                                     28 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 87
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94.8%; Score 851; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.2e-98;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                  94.8%; Score 851; DB 2; I 100.0%; Pred. No. 2.2e-98;
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94.8%; Score 851; UB
Best Local Similarity 100.0%; Pred. No. 2.2
Matches 166; Conservative 0; Mismatches
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Patent No. 6426042
GENERAL INFORMATION:
AFPLICANT: Asada, Kiyozo
TELECOMMUNICATION INFORMATION:
            TELEPHONE: (416) 364-7311
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 amino acids
                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                           amino acid
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US-09-366-009-34
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-09-552-265B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                 Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1-999
CLASSIFICATION AUMBER: 08/809,156
FILING DATE: (UNKNOWN)
APPLICATION NUMBER: 08/809,156
FILING DATE: 4UNKNOWN APPLICATION NUMBER: UP 294382/1995
FILING DATE: 13-NOV-1-995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser. Gerard J.
REPERRENCE/DOCKET NUMBER: 19,763
REPERRENCE/DOCKET NUMBER: 19,763
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-366-009-34
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
APPLICANT: Uemori, Takashi
APPLICANT: Ueno, Takashi
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
Uemori, Takashi
Ueno, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 SECUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.4
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                 NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-809-156B-34
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us-10-014-363-5.rai

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69 VEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGIRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                          Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                   94.2%; Score 846; DB 3; 100.0%; Pred. No. 7.2e-98; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09604938

Patent No. 6583272

GENERAL INFORMATION:
APPLICANT: Ballon, Pascal
TITLE OF INVENTION:
FILE REPERENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/09/604,938

CURRENT FILING DATE: 2000-06-27

PRIOR APPLICATION NUMBER: 60/166,151
PRIOR APPLICATION NUMBER: 60/166,151
PRIOR APPLICATION NUMBER: 60/165,151
PRIOR APPLICATION NUMBER: 60/151,548

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: 60/150,225

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-23

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

SOFTWARE: PLANCY DATE: 1999-07-02

INWER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.2%; Score 846; DB 4;
    FILE REFERENCE: 1098 nonprovisional CURRENT APPLICATION NUMBER: US/09/604,871 CURRENT FILING DATE: 200-06-28 PRIOR APPLICATION NUMBER: 60/151,454 PRIOR FILING DATE: 1999-08-30 PRIOR FILING DATE: 1999-08-05 PRIOR FILING DATE: 1999-08-05 PRIOR FILING DATE: 1999-07-02 PRIOR FILING DATE: 1999-07-02 NUMBER OF SEQ ID NOS: 3 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                 LENGTH: 165
                                                                                                                                                                                                                                                                                                                                                   US-09-604-871-1
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Pred. No. 1.7e-97;
1; Mismatches 0; Indels
           APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
TITLE OF INVENTION: CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IS Floppy disk

SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,156B

FLING DATE: 07-MAR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/02254

FLING DATE: 13-NOV-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 294382/1995

FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 51847/1996

FILING DATE: 08-MAR-1996

ATTONERY/AGENT INPOMMATION:

NAMMP: Washer Canarada
                                                                                                                                                   ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
Koyama, No. 6472204uto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 412 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.4<sup>1</sup>
Matches 165, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                             PA
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US-09-604-871-1
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Gaps

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                                                                                 1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                             9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                   0; Gaps
Length 165;
                                                                                                                                                                                                   129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 173
            100.0%; Pred. No. 7.2e-98; ive 0; Mismatches 0; Indels
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Sequence 1, Application US/09604871
Patent No. 6340742
GRNERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Hilger, Bernd
APPLICANT: Josel, Hans-Peter
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES

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APPLICATION NUMBER: PCT/GB98/03449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09552265B
; Patent No. 6555343
                                                                                                                                    LENGTH: 165 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: DeSauvage, Frederick
                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.9%;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 164; Conservative
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Best Local Similarity 99.4
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-552-265B-2
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APPLICANT: Sterrenheld Biotechnologie No. 6777205th America, Inc.
APPLICANT: Carcagno, Carlos Miguel
APPLICANT: Criscuolo, Marcelo
APPLICANT: Melo, Carlos Miguel
APPLICANT: Melo, Carlos Barcesing Recombinant Human Erythropoietin
FILE REFERENCE: 1999-1029 002009 967
CURRENT APPLICATION NUMBER: US/09/830,967
CURRENT PILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: AR 99-01-00679
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGGQA 60
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    PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anthony ATKINSON
TITLE OF INVENTION: Detection of Molecules in Samples NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/554,451
FILING DATE: 15-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WOR'D CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jonathan Paul MURPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09554451 Patent No. 6680207 GENERAL INFORMATION:
                                                                                                                                        Sequence 1, Application US/09830967
Patent No. 6777205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
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US-09-554-451-8
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LENGTH: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Honor: Dennis, J.
TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
TITLE OF INVENTION: polypetides and nucleic acids encoding the same FILE REPERENCE: GENENT.057CPl
CURRENT APPLICATION NUMBER: US 09/552,265B
CURRENT FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: US 09/307307
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                :
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Pred. No. 2.2e-97;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 843; DB 4; Length 165;
Pred. No. 1.7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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FILING DATE: No. 6680207ember 16, 1998
APPLICATION NUMBER: GB 9723955.2
FILING DATE: No. 6680207ember 14, 1997
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                              TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-554-451-8
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November 19, 2004, 21:11:10; Search time 82.4565 Seconds (without alignments) 747.281 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                              1 APPGAAHYAPPRLICDSRVL.......NFLRGKLKLYTGEACRTGDR 174
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/ Cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
/ Cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
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/ Cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
/ Cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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/ Cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ Cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
/ Cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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length: 2000000000
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Maximum DB seq
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	Description	100 110 110 110 110 110 110 110 110 110	Section of a concernor	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	'n	o,	Sequence 2, Appli	Sequence 2, Appli	Sequence 227, App	Sequence 1, Appli	sequence 201, App
SUMMARIES	ID		US-10-014-363-5	US-10-014-363-3	US-10-014-363-4	IIS-09-853-731-7	11S-10-014-363-7	2-595-FTO OT CO	TIG-10-005 CE1 0	TG-10 400 222 0	116-10-400-3//-Z	TIS-10-208-2	TS-10-250-148-2	TS-10-360-101-22/	.5 03-10-46/-TIS-I 6 US-10-658-8348-201	T07-WFC9-9C9 07 00
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ALIGNMENTS

0 61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120 61 RMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRAL 120 9 1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVEDTKVNFYAWK Gaps 0 Length 174; Indels 100.0%; Score 898; DB 13; 100.0%; Pred. No. 1.4e-90; Live 0; Mismatches 0; APPLICANT: Burg, Josef
APPLICANT: Bragel, Alfred
APPLICANT: France, Reinhard
APPLICANT: France, Reinhard
APPLICANT: Higer, Bernd
APPLICANT: Tischer, Wilhelm
APPLICANT: Worny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805 CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5 ; Sequence 5, Application US/10014363; Publication No. US20020115833A1; GENERAL INFORMATION: Query Match
Best Local Similarity 100.
Matches 174; Conservative ; TYPE: PRT ; ORGANISM: CHO/dhfr-US-10-014-363-5 LENGTH: 174 ð qq ਨੇ qq

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69 VEVWOGLALLSEAVIRGOALLVNSSQPWEPLOLHVDKAVSGLRSLITILLRALGAQKEAIS 128
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      1 APPGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWK
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                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09853731

Sequence 2, Application US/09853731

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Erythropoietin Composition
TITLE FEFFENCE: 20619 US
CURRENT FAPPLICATION NUMBER: US/09/853,731

CURRENT FILING DATE: 2001-05-11

PRIOR FILING DATE: 2000-05-15

PRIOR FILING DATE: 2000-05-15

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10014363
; Publication No. US2020115833A1
; Publication No. US2020115833A1
; GENERAL INFORMATION:
APPLICANT: Burg, Josef
APPLICANT: Brigel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Hilger, Bernd
APPLICANT: Tischer, Wilhelm
APPLICANT: Schurig, Hartmut Brnst
APPLICANT: Schurig, Hartmut Brnst
APPLICANT: Schurig, Hartmut Brnst
APPLICANT: Wozny, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT APPLICATION NUMBER: US/10/014,363
CURRENT FILING DATE: 2001-12-11
SOFFWANDEN OF SEQ ID NOS: 5
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-853-731-2
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LENGTH: 166
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US-09-853-731-2
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Best Local Similarity 97.1%; Pred. No. 1.7e-86;
Matches 169; Conservative 0; Mismatches 5; Indels
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APPLICANT: Engel, Alfred
APPLICANT: Franze, Reinhard
APPLICANT: Franze, Reinhard
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Schurig, Hartmut Ernst
APPLICANT: Tischer, Wilhelm
APPLICANT: Wozhy, Manfred
TITLE OF INVENTION: Erythropoietin Conjugates
FILE REFERENCE: Case 20805
CURRENT PRILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
                                                                                                                                   Sequence 3, Application US/10014363

Publication No. US20020115833A1

GENERAL INFORMATION:

APPLICANT: Burg, Josef

APPLICANT: Franze, Reinhard

APPLICANT: Hilger, Bernd

APPLICANT: Tischer, Marthut Ernst

APPLICANT: Tischer, Wilhelm

APPLICANT: Wozny, Manfred

TITLE NO INVENTION: Erythropoietin Conjugates

FILE REFERENCE: Case 20805

CURRENT APPLICATION NUMBER: US/10/014,363

CURRENT FILING DATE: 2001-12-11

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin version 3.1
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Best Local Similarity 97.1
Matches 169; Conservative
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ORGANISM: CHO/dhfr-
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LENGTH: 174
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                                                                                                        9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                                                                                                               1 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDIKVNPYAWKRMEVGQQA 60
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                                     Score 851; DB 13; Length 166;
Pred. No. 2e-85;
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94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels (
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                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10241356; Publication No. US20030077753A1; GENERAL INFORMATION:
GENERAL INFORMATION:
FILE OF INVENTION: DIGLYCOSYLATED ERYTHROPOLETIN; FILE REFERENCE: 20971
CURRENT FILING DATE: 2002-09-11; PRIOR APPLICATION NUMBER: US/10/241,356; CURRENT FILING DATE: 2001-09-25; NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/1029351
Publication No. US2003012004541
GENERAL INFORMATION:
APPLICANT: Bailon, Descal
TITLE OF INVENTION: ERYTHROPOIETIN CONJUGATES
FILE REFRENCE: 1097 nonprovisional
CURRENT APPLICATION NUMBER: US/10/293,551
CURRENT FILING DATE: 2002-11-14
FRIOR FILING DATE: 2000-06-27
FRIOR APPLICATION NUMBER: 06/166,151
FRIOR APPLICATION NUMBER: 60/161,54
FRIOR FILING DATE: 1999-11-17
FRIOR FILING DATE: 1999-11-17
FRIOR FILING DATE: 1999-11-17
FRIOR FILING DATE: 1999-11-17
FRIOR FILING DATE: 1999-08-13
FRIOR FILING DATE: 1999-08-13
                      94.8%; Scor.
100.0%; Pred. No. co.
                               Query Match
Best Local Similarity 100.
Matches 166; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 166
US-10-014-363-2
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US-10-293-551-2
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Publication No. US20030162949A1

GENERAL INFORMATION:

APPLICANT: Cox III, George N

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins

TITLE REPRENCE: 4152-1-FUS

CURRENT APPLICATION NUMBER: US/10/400,377

CURRENT FILING DATE: 2003-03-26

PRIOR FILING DATE: 2000-01-14

PRIOR FILING DATE: 1997-07-14
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100.0%; Pred. No. 2e-85;
tive 0; Mismatches 0; Indels (
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PRIOR FILING DATE: 1999-08-23
PRIOR APPLICATION NUMBER: 60/142,254
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 166
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 166
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US-10-293-551-2
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Best Local Similarity
Matches 166; Conserv
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Sequence 2, Application US/10298148

Publication No. US20030171284A1

GENERAL INFORMATION:
APPLICANT: COX III, George N

APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-Pug

CURRENT APPLICATION NUMBER: US/10/298,148

CURRENT FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US/09/462,941

PRIOR APPLICATION NUMBER: 60/052,516

PRIOR PILING DATE: 1997-07-14

PRIOR PILING DATE: 1997-07-14

NUMBER OF SEQ ID NOS: 41

SOCFWARE: Patentin Ver. 2.0
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APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REPERENCE: 4152-1-P0G
CURRENT APPLICATION NUMBER: US/10/400,708
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1907-07-14
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.0
SSEQ ID NO 2
LENGTH: 166
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94.8%; Score 851; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                 94.8%; Score 851; DB 14; Length 166; 100.0%; Pred. No. 2e-85; 1ve 0; Mismatches 0; Indels
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Matches 166, Conservative
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US-10-298-148-2
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US-10-298-148-2
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APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornelis J.
TILE CONTRIBUTION: Export and modification of (poly) peptide in the lantibiotic way FILE REPERINCE: 2183-5673
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US/10/360,101
PRIOR APPLICATION NUMBER: BP 02077060.8
PRIOR APPLICATION NUMBER: BP 02077060.8
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 227
LENGTH: 166
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100.0%; Pred. No. 2e-85;
Live 0; Mismatches 0; Indels
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Sequence 1, Application US/10467115
Publication No. US20040063917A1
GENERAL INPORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Carr, Graham
APPLICANT: Carr, Graham
APPLICANT: Williams, Stephen
TITLE OF INVENTION: DOIFIED ERYTHROPOIETIN (EPO) WITH
TITLE OF INVENTION: REDUCED IMMUNGENICITY
FILE REFERENCE: MEEL 114
CURRENT APPLICATION NUMBER: US/10/467,115
CURRENT FILING DATE: 2003-08-05
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 166
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94.8%; Score 851; DB 15; Length 1
Best Local Similarity 100.0%; Pred. No. 2e-85;
Matches 166; Conservative 0; Mismatches 0; Indels
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; Sequence 227, Application US/10360101; Publication No. US20040009550A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 166; Conservative
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ORGANISM: Homo Sapien
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61 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGIRSLTTLLRALGAQKEAIS 120
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APPLICANT: Cox III, George N
TITLE Bolder Biotechnology, Inc.
TITLE POINTENER: 415-1-4103
CURRENT FILING DATE: 2004-02-05
FILE REPLICATION NUMBER: US/10/774,149
CURRENT FILING DATE: 2004-02-05
FRIOR APPLICATION NUMBER: US/09/462,941
FRIOR FILING DATE: 2003-03-26
FRIOR FILING DATE: 109/0-01-14
FRIOR FILING DATE: 2000-01-14
FRIOR FILING DATE: 109/0-01-14
FRIOR FILING DATE: 109/0-01-14
FRIOR FILING DATE: 109/0-01-14
FRIOR FILING DATE: 109/0-01-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 166;
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Pred. No. 2e-85;
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ilarity 100.0%; Pred. No. 2e-85;
Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US/09/462,941
PRIOR FILING DATE: 2000-01-14
PRIOR FILING DATE: 1997-07-14
NUMBER OF SEQ ID NOS: 41
SOUTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10774149
Publication No. US20040175800A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 166; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                   LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                              US-10-773-939-2
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                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ## Sequence 201, Application US/10658834A

| Sequence 201, Application US/10658834A
| Sequence 201, Application No. US20040132977A1
| Gandarion No. US20040132977A1
| APPLICANT: Gantier, Rene
| APPLICANT: Guyon, Thierry
| APPLICANT: Oritianal Evolution of Cytokines for Higher Stability, Encoding Nu TILLE OF INVENTION: Acid
| TITLE OF INVENTION: Acid
| FILE REFERENCE: 38751-922
| CURRENT APPLICATION NUMBER: US/10/658,834A
| FRIOR PLILING DATE: 2003-09-08
| PRIOR APPLICATION NUMBER: 60/457,135
| PRIOR APPLICATION NUMBER: 60/457,135
| PRIOR APPLICATION NUMBER: 60/409,898
| PRIOR APPLICATION NUMBER: 60/409,898
| PRIOR PLING DATE: 2002-09-09
| NUMBER OF SEQ ID NOS: 1306
| SEQ ID NO 201
| LENCTH: 166
                                                                                                                                                 69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                            69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                    9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Publication No US20040175356A1
GENERAL INFORMATION:
APPLICANT: Cox III, George N
APPLICANT: Bolder Biotechnology, Inc.
APPLICANT: Bolder Biotechnology, Inc.
TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
FILE REFERENCE: 4152-1-DUS
CURRENT APPLICATION NUMBER: US/10/773,939
PRIOR APPLICATION NUMBER: US/10/400,377
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100.0%; Pred. No. 2e-85;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                   129 PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AAA52400
DATABASE ENTRY DATE: 1994-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166; Conservative
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Best Local Similarity
Matches 166; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-658-834A-201
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Job time : 83.4565 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

; Search time 20.1934 Seconds November 19, 2004, 20:59:24 Run on:

(without alignments) 829.068 Million cell updates/sec

1 APPGAAHYAPPRLICDSRVL.......NFLRGKLKLYTGEACRTGDR 174 Perfect score:

US-10-014-363-5

Seguence:

**BLOSUM62** 

Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR 79:\* Database

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

erythropoietin pre erythropoietin pre erythropoietin - r erythropoietin - p erythropoietin - d thrombopoietin - h ribonucleoside-dip Solute binding rec megakaryocyte grow UDP-N-acetylpyruvo hypothetical prote ATP-dependent Clp erythropoietin pre thrombopoietin pre genome polyprotein bacterioferritin X probable sensory h ABC transporter AT ATP-dependent heli EGF receptor subst conserved hypothet methylamine utiliz probable copper-tr probable 2-hydroxy ribosomal protein erythropoietin erythropoietin erythropoietin Description SUMMARIES 146199 G02729 180105 AB0323 AE0959 AB3274 AB3274 AR3274 GNWV43 GNWV63 S56639 T35450 AF0526 184613 146083 S28148 A24902 JC7699 I46578 AG2919 H97693 D75500 146401 T35681 454696 Query Match Length DB 78.6 76.9 76.4 76.1 76.1 71.0  $\begin{smallmatrix} \mathbf{w} & \mathbf{w}$ 851 765.5 765.5 718 706 690.5 686 87.5 86 85 83.5 80.5 79.5 79.5 79.5 79.5 78.5 78.5 78.5 78 78 Score 88 88 683 638 Result Ño.

hypothetical prote	hypothetical prote	60 kD chaperonin (	g - This uinoidmys	mandelate racemase	groEL protein - Ba	hypothetical prote	conserved hypothet	rtS beta (AF305057	ATP-dependent heli	RF2 protein - saim	thrombopoietin pre	ribonucleoside-dip	hypothetical profe	chaperonin, 60 Kd	9
AD1928	875569	B84932	B42281	AE3465	837039	875772	AB2922	C97696	D64738	B37994	JC4125	AH3625	A75537	B82048	839765
~1	~	~	~	~	7	7	7	7	7	7	~	~	~	7	7
242	451	548	548	425	544	637	400	425	824	282	326	335	347	544	552
9.6	9.8	8.6	8.6	8.5	8.4	8.4	8.3	8.3	8.3	8.2	8.2	8.2	8.2	8.2	8.2
77.5	77	77	77	76.5	75.5	75.5	74.5	74.5	74.5	74	74	74	74	74	74

## ALIGNMENTS

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R.J.; Mufson, A.; See erythropoietin precursor [validated] - human C;Species: Homo sapiens (man) C;Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text\_change 09-Jul-2004 C;Accession: A01855, A247444; A25384; A22210; S56178 K;Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Murure 313, 806-810, 1985

A;Title: Isolation and characterization of genomic and cDNA clones of human erythropoiet A;Reference number: A01855; MUID:85137899; PMID:3838366

A; Accession: A01855

A; Molecule type: mRNA; DNA
A; Residues: 1-193 «JAC.
B; Lin, C.H.; Browne, J.K.; Smalling, R.; Egrie, J.C.; Chen, K.K.; Proc. Natl. Acad. Sci. U.S.A. 82, 7580-7584, 1985
A; Title: Cloning and expression of the human erythropoietin gene.
A; Reference number: A24744; MUID:86067948; PMID:3865178
A; Recession: A24744
A; References: GB:M11319; NID:9182197; PIDN:AAA52400.1; PID:9182198
A; Residues: 1-133 «LIN»
A; Cross-references: GB:M11319; NID:9182197; PIDN:AAA52400.1; PID:9182198
A; Rilai, P.H.; Everett, R.; Wang, F.F.; Arakawa, T.; Goldwasser, E.
A; Title: Structural characterization of human erythropoietin.
A; Reference number: A25384; MUID:86140080; PMID:3949763

A;Accession: A25384

pre

Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: 28-86, Cv, 87-193
Ajmolecule type: 28-86, Cv, 87-193
Ajmolecule type: protein unit cance; uring source: ur

A;Accession: A22210
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: 28-29, X', 31-33, 'L', 35-50, 'X', 52-53, 'D', 55, 'G', 57 <YAN>
R;Matsumoto, S.; Ikura, K.; Udda, M.; Sasaki, R.
Plant Mol. Biol. 27, 1163-1172, 1995
A;Title: Characterization of a human glycoprotein (erythropoietin) produced in cultured A;Reference number: S56178; MUID:95284365; PMID:7766897

A; Accession: S56178

A,Molecule type: protein A,Molecule type: 28-33, X',35-37 <MTS> A,Residues: 28-33, X',35-37 <MTS> C,Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver o A,Gene: GDB:EPO A;Cross-references: GDB:119110; OMIM:133170

A,Map position: 7q21.3-7q22.1 A,Introns: 5/1; 53/3; 82/3; 142/3

C; Function

C;Species: Macaca mulatta (rhesus macaque)

A; Description: the primary inducer of erythrocyte formation

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C.Date: 02-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C.Accession: 184613
R.Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A.Title: Brythropoietin structure-function relationships: High degree of sequence homology. A.Reference number: 146083; MUID:93372347; PMID:8364201
                                                                                                                                                                                                                                     A)Cross-references: UNIPROT:028513; GB:L10609; NID:g342095; PIDN:AAA36842.1; PID:g342096
C)Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver C
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 193
A;Title: Brythropoietin structure-function relationships: High degree of sequence homolo
A;Reference number: 146083; MUID:93372347; PMID:8364201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-188 <WEN>
A;Cross-references: UNIPROT: P33708; GB:L10606; NID:g163820; PIDN:AAA30807.1; PID:g163821
C;Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVGOOAVEVWOGLALLSEAVLRGOALLVNSSOPWEPLOLHVDKAVSGLRSLTTLLRALGA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erythropoietin precursor - cat (fragment)
C;Species: Pelis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: 146083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PGAAHYAPPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRM
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                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: erythropoietin

Keywords: erythropoissis; glycoprotein; hormone; kidney; liver

F;1-27/Domain: signal sequence #status predicted <51G>

F;28-192/Product: erythropoietin #status predicted <MAT>

F;34-187,56-60/Disulfide bonds: #status predicted

F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;152/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.2%; Score 765.5; DB 1; Length 192; 88.4%; Pred. No. 2.2e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 718; DB 1; Length 18 Pred. No. 7.2e-61; 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                         A, Description: the primary inducer of erythrocyte formation
                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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ilarity 84.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                           A; Accession: I84613
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R;Lin, F.K.; Lin, C.H.; Lai, P.H.; Browne, J.K.; Egrie, J.C.; Smalling, R.; Fox, G.M.; Gene 44, 201-209, 1986
A;Title: Monkey erythropoietin gene: cloning, expression and comparison with the human A; Reference number: JQ0173; MUID:87055236; PMID:2877922
A; Accession: JQ0173
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                                                                                                                                                                                                                                                                                                                                                                                                                                         VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
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                                                                                                                                                                                                                                                                                                                                                                       APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 87
             C;Superfamily: erythropoietin
C;Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
C;Keywords: erythropoiesis; glycoproteid <6SIG>
F;128-193/Product: erythropoietin #status experimental <MAT>
F;38-193/Product: erythropoietin #status experimental
F;34-188;56-60/Disulfide bonds: #status experimental
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;153/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erythropoietin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                   9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Pred. No. 7.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGBACRTGDR 193
                                                                                                                                                                                                                          Query Match 94.8%; Score 851; DB 1; Length 193; Best Local Similarity 100.0%; Pred. No. 1.7e-73; Matches 166; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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ilarity 89.5%;
Conservative 7
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Best Local Similarity
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R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoletin structure-function relationships: High degree of sequence homolo A;Reference number: 146083; MUID:93372347; PMID:8364201
                      Cross-references: UNIPROT:P33709; EMBL:Z24681; NID:g395049; PIDN:CAA80848.1; PID:g395
                                                                                                                                                                                   A;Status: translated from GB/EMBL/DDBJ
A; Residues: 1-194 <FUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A24902
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A, Status: translated from GB/EMBL/DDBJ
A, Cross-references: GB:L10608; NID:g204060; PIDN:AAA41126.1; PID:g204061
C, Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver of shortion: the primary inducer of erythrocyte formation
C, Superfamily: erythropoietin is produced; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted calco
F;27-192/Product: erythropoietin #status predicted
F;33-187,55-165/Disulfide bonds: #status predicted
F;50.64,109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                               C; Species: Rattus norvegicus (Norway rat)
C; Spate: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C; Jate: 22-Nov-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C; Accession: S28148; 162743
R; Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikura, K.; Sasaki, R. Biochim. Biophys. Acta 1171, 99-102, 1992
Biochim. Biophys. Acta 1171, 99-102, 1992
A; Title: Nucleotide sequence of rat erythropoietin.
A; Reference number: S28148; MUID:93042015; PMID:1420369
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                                          69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                    PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                     129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.6%; Score 706; DB
82.5%; Pred. No. 1e-5
live 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wen, D.; Boissel, J.
Blood 82, 1507-1516, 1993
A;Title: Erythropoietin structure-function
A;Reference number: 146083; MUID:93372347;
                                                                                                                                                                                                                                                                                                            erythropoietin precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.59
Matches 137; Conservative
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A; Residues: 1-192 <NAG>
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A.Molecule type: mRNA
A.Residues: 4-15,'L'.17-107,'P',109-194 <WEN>
A.Cross-references: GB:L10610; NID:g165876; PIDN:AAA31518.1; PID:g165877
C.Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the mouse erythropoietin gene
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A;Molecule type: DNA
A;Residues: 1-6/, P', 69-192 <MCD>
A;Coss-references: GB:M12930; NID:g193086; PIDN:AAA37570.1; PID:g387152
C;Comment: Brythropoietin is produced by kidney or liver of adult mammals and by liver of C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 erythropoietin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 APPKLICDSRVLERYILEAREAENAIMGCAEGCSFSENIIVPDTKVNFYAWKRMEVQQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                            C; Keywords: erythropolesis; glycoprotein; hormone; kidney; liver
F;1-27/Domain: signal sequence #status predicted <81G>
F;28-194/Product: erythropoletin #status predicted <MAT>
F;34-189,56-60/Disulfide bonds: #status predicted
F;51,65,110/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;154/Binding site: carbohydrate (Ser) (covalent) #status predicted
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G;Function: A;Description: the primary inducer of erythrocyte formation C;Superfamily: erythropoietin
C;Keywords: erythropoietin
C;Keywords: erythropoietis; glycoprotein; hormone; kidney; liver
F;1-26/Domain: signal sequence #status predicted cSIGs
F;27-192/Product: erythropoietin #status predicted cMAT>
F;33-187,55-165/Disulfide bonds: #status predicted
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A, Residues: 1-192 <SHO.
A, Residues: 1-192 <SHO.
A, Cross-references: UNIPROT: P07321
A, Cross-references: UNIPROT: P07321
A, Note: the authors translated the codon TTA for residue 12 as R, McDonald, J.D.; Lin, F.K.; Goldwasser, E.
Mol. Cell. Biol. 6, 842-848, 1986
A, Title: Cloning, sequencing, and evolutionary analysis of the A, Reference number: A24901; MUID: 87039104; PMID: 3022133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: the primary inducer of erythrocyte formation C; Superfamily: erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A24902; A24901
R;Shoemaker, C.B.; Mitsock, D.D.
Mol. Cell. Biol. 6, 849-889, 1986
A;Title: Muxine erythropoietin gene: cloning, expression,
A;Reference number: A24902; MUID:87039105; PMID:3773894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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9; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.9%; Score 690.5; Best Local Similarity 82.0%; Pred. No. 3.10 Matches 137; Conservative 9; Mismatches
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 16-Aug-1996 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: 146401; 147077
R;Fu, P.; Evans, B.; Lim, G.B.; Moritz, K.; Wintour, E.M.
Mol. Cell. Endocrinol. 93, 107-116, 1993
A;Title: The sheep erythropoietin gene: molecular cloning and effect of hemorrhage on FAReference number: 146401; MUID:93351736; PMID:8349021
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A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA

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A,Residues: 1-175 <WEN>
A,Cross-references: UNIPROT: P33707; GB:L13027; NID:g290087; PIDN:AAA30842.1; PID:g552347
C;Superfamily: erythropoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 VEVWOCHALLSEAVLRCGALLVNSSOPWEPLOLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                23 APPRLICDSRVLERYILEAREABNVTWGCAQGCSFSENITVEDTKVNFYTWKRMDVGQQA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-353 < IMX.
A; Cross-tréerences: EMBL: U59493; NID: g1401245; PIDN: AAB03392.1; PID: g1401246
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erythropoietin - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: I46199
R;Wen, D; Boissel, J.
Blood 82, 1507-1516, 1993
A;Fitle: Erythropoietin structure-function relationships: High degree of seq A;Reference number: I46083; MUID:93372347; PMID:8364201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G02729
R;Im, S.
                                                                                                                                        23 APPRLICDSRVLERYILEAKEGENATWGCAESCSFSENITVPDTKVNFYAWKRWEVQQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSINENITVPDTKVNFYAWKRMEVGQQA
                                                                                                            9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                  143 LPDASPSSATPLRTFAVDTLCKLFRNYSNFLRGKLTLYTGEACRRRDR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.0%; Score 638; DB 2; Length 175; 81.0%; Pred. No. 2.7e-53;
            Length 190;
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                                                                                                                                                                                                                                                                                                           129 PPDA--ASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
               Score 683; DB 2;
Pred. No. 1.5e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, May 1996
A;Reference number: H01637
A;Accession: G02729
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKL 161
76.1%; Sco...
82.1%; Pred. No. 1...
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches
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Best Local Similarity 81.03
Matches 124; Conservative
                    Query Match
Best Local Similarity 82.1
Matches 138; Conservative
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Best Local Similarity
Matches 41; Conserva
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: 30-Sep-2001 #sagalith, M.; Hobart, P.
Biochem. Biophys. Res. Commun. 284, 83-827, 2001
A;Tille: Rabbit EPO gene and cDMA: Expression of rabbit EPO after intramuscular injectic
A;Cession: 30-7699; MUID:21290682; PMID:11396976
A;Cossion: 30-7699
A;Molecule type: DNA
A;Residues: 1-195 <VII.>
A;Cossion: 30-7699
A;Molecule type: DNA
A;Residues: 1-195 <VII.>
A;Cromment: This protein, a heavily glycosylated 34K protein produced in the fetal liver
C;Genetics:
C;Genetics:
A;Gene: epo
C;Superfamily: erythropoietin
C;Keywords: glycoprotein; kidney
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Blood 82, 1507-1516, 193
Blood 82, 1507-1516, 193
A;Title: Brythropoietin structure-function relationships: High degree of sequence homolc A;Reference number: 146083; MUID:93372347; PMID:8364201
A;Accession: 146578
A;Accession: preliminary, translated from GB/EMBL/DDBJ
A;Relecule type: mRNA
A;Residues: 1-190 < WEN>
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C;Superfamily: erythropoietin
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                                                                                                                                                                                                                                                 69 VEVWQGLALLSEAVIRGQALLVNSSQPWEPLQLHVDKAVSGIRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                 69 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 APARLICDSRVLERYILEAKBAENVTMGCAEGCSLGENITVPDTKVNFHHWKKSEAGRHA 88
                                                                                                                      68
                                                                                                                                                                      98
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                  9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                         147 PPDTTPPAPLRTLTVDTFCKLFRVYANFLRGKLKLYTGFVCRRGDR 192
                                                                                                                                                                                                                                                                                                                129 PPDAASAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
                    Length 192;
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                                                                    20; Indels
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; Pred. No. 9.2e-58;
12; Mismatches 18
                      Query Match 76.4%; Score 686; DB 1; Best Local Similarity 79.5%; Pred. No. 8.1e-58; Matches 132; Conservative 14; Mismatches 20.
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Best Local Similarity
Matches 136; Conserv
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-323 <KUR>
A,Cross-references: UNIPROT:Q8ZDC8; GB:AL590842; PIDN:CAC92889.1; PID:g15980631; GSPDB:G
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta chain [imported] - Yersinia pest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Solute binding receptor protein [imported] - Salmonella enterica subsp. enterica serovar C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: A80323 Wen, B. W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Reakfull, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M. Atture 413, 523-527, 2001

A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 VEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 NITVPDTKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVD- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 ---KAVSGLRSLTTLLRALGAQ---KEAISPPDAASAAPLRTITADTFRKLFRVYSNFLR 158
                                                                                                                                                                                                                                                                                                                                         68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                              9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                          22; Gaps
                                                                                                                                                                                                  Length 353;
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                                           A;Map position: 3q26.3-3q27
A;Introns: 5/1; 47/3; 76/3; 132/3
C;Keywords: alternative splicing; cytokine; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: nrdF
C;Superfamily: ribonucleoside-diphosphate reductase beta
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 ISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                            41; Conservative 20; Mismatches
                                                                                                                                                                                          9.9%; Score 89; 26.3%; Pred. No.
              A;Cross-references: GDB:374007; OMIM:600044
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                                                                                                                                                                                   Query Match
Best Local Similarity
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A/Golecule type: DNA
A/Residues: 1-353 <RE2>
A/GCOSS-references: UNIPROT:P40225; GB:L36051; NID:g533214; PIDN:AAC37568.1; PID:g533215
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A/Cross-references: GB:L36052; NID:g533216; PIDN:AAC37566.1; PID:g533217
B/G Sauvage, F.J.; Hass, P.E.; Spencer, S.D.; Malloy, B.E.; Gurney, A.L.; Spencer, S.A.
D.V.; Eaton, D.L.
Nature 369, 533-538, 1994
A/Title: Stimulation of megakaryocytopoiesis and thrombopoiesis by the c-Mpl ligand.
A/Reference number: 845331
A/Stetus: preliminary
A/Molecule type: mRNA
A/Residues: 1-353 <AUSA
A/Reference number: S48740; MUID:95010765; PMID:7926023
A/Reference number: S48740; MUID:95010765; PMID:7926023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombopoietin precursor - human

N.Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor

N.Alternate names: c-MPL ligand; megakaryocyte growth and development factor precursor

S.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.Spacies: Homo sapiens (man)

C.Spacies: Homo sapiens (man)

C.Spacies: J. Hould (man)

A.Title: Human thrombopoietin: gene structure, CDNA sequence, expression, and chromosomal (man)

A.Title: Human thrombopoietin: gene structure, CDNA sequence, expression, and chromosomal (man)

A.Title: Human thrombopoietin: gene structure, CDNA sequence, expression, and chromosomal (man)
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A; Crosdives: 1-353 < SOH3-
A; Crosdives: 1-353 < SOH3-
B; Bartley, T.D.; Bogenberger, J.; Hunt, P.; Li, Y.S.; Lu, H.S.; Martin, F.; Chang, M.S.;
A; Title: Identification and cloning of a megakaryocyte growth and development factor tha
A; Reference number: A54463; MUID:94291201; PMID:8020099
A; Accession: I38672
A; Accession: I38672
A; Molecule type: mRNA
A; Residues: 1-112, E', 114-353 < RE3>
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A;Accession: 152610
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R;Gurney, A.L.; Kuang, W.J.; Xie, M.H.; Malloy, B.E.; Eaton, D.L.; de Sauvage, F.J.
                                                                                                                                   69 VEVWQGLALLSEAVL--RGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA 126
                                                                                                                                                                                       ODILGAVTLILEGYWAARGQLGPTCLSSILGQLSEQVRILLGALQSL-----LGTQ--- 132
9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 68
                                           24 APP--ACDLRVLSKLLRDSHVLHSKLSQCPEVHPLPTPVLLPAVDFSLGEWKTQMEETKA 81
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                                                                                                                                                                                                                                                                               127 ISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLK 162
                                                                                                                                                                                                                                                                                                                                                 -LPPOG-----RTTAHKDPNAIFLSFQHLLRGKVR 161
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A;Molecule type: DNA
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A,Status: translated from GB/EMBL/DDBJ
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lood 85, 981-988, 1995
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A, Status: preliminary
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megakaryocyte growth and development factor, long form - human
MiAlternate names: MPL ligand, long form
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: A55530
R;Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.; Perkins, C.; Mar, V.; Suggs, S
J. Balol. Chem. 270, 511-514, 1995
A;Title: Cloning and characterization of the human megakoryocyte growth and development
A;Reference number: A55530, MUID:95122483; PMID:7822271
A;Accession: A55530
A;Accession: A55530
A;Ketus: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Cross-references: GB:U17071
C;Genetics:
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: ABO502; MUD:21534947; PMID:11677608
A;Accession: AE0559
A;Status: preliminary
A;Status: preliminary
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A;Residues: 1-346 <PAR>
A;Crosar-references: GB:AL513382; PIDN:CAD03169.1; PID:g16504804; GSPDB:GN00176
C;Genetics:
A;Gene: STY3952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 QDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLLLGALQSL-----LGTQ--- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GLALLSEAVIRGOALLVNSSQ-PWEPLQLHVDKAVSGLRSLTTLLRALGAQ--KEAISPP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 APP--ACDLRVLSKLIRDSHVIHSRLSQCPEVHPLPTFVLLPAVDFSLGEWKTQMEETKA 81
                                                                                                                                                                                                                                                                                                                                                                                                                     18 RVLERYLLEAKEAENITTG--CAEHCSLNE--NITVPDTKVNFYAWKRMEVGQQAVEVWQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Gaps
                                                                                                                                                                                                                                                                                                  9.7%; Score 87.5; DB 2; Length 346; 26.7%; Pred. No. 1.4; tive 22; Mismatches 48; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.6%; Score 86; DB 2; Length 286; Best Local Similarity 26.6%; Pred. No. 1.5; Matches 41; Conservative 18; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 -----DAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         310 VLILTHNNADSARVRRSLSPPGFRPVY-----LYQYTSEA 344
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A.Map position: 3q26.3
C.Keywords: alternative splicing; cytokine
                                                                                                                                                                                                                                                                                                                                Best Local Similarity 26.7%
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                        Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 19, 2004, 20:59:03; Search time 103.996 Seconds (without alignments) 962.682 Million cell updates/sec Run on:

Title: Perfect score:

US-10-014-363-5 898 1 APPGAAHYAPPRLICDSRVL.....NFLRGKLKLYTGEACRTGDR 174 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

88		Description	P01588 homo sapien	Aap22357 homo gapi		macaca	ednns	felis	rattus	Q6pwu5 canis famil	~	P48617 bos taurus	P07321 mus musculu	ovis		099ka3 oryctolagus		spalax	_	Q6h8t1 spalax carm						Q8hz87 pongo pygma		Baquin	Н	Aar25698 tetraodon	O6iv23 fugu rubrip	Aag72466 fugu rubr	Q6jv22 fugu rubrip
SUMMARIES		ai ei	EPO HUMAN	AAP22357	EPO MACFA	EPO MACMU	Q867B1	EPO FELCA	EPO_RAT	Q6PWU5	AAS77874	EPO BOVIN	EPO MOUSE	EPO_SHEEP	Q9GKA2	Q9GKA3	EPO PIG	Q6H8S9	Оенвто	Q6H8T1	Q9MYM8	Q6H8T2	QBHZ88	Q8HZ89	EPO_CANFA	Q8HZ87	98ZH8Q	Q8HZ85	Q6UAM1	AAR25698	Q6JV23	AAQ72466	Q6JV22
		DB	н	~	7	-	7		Н	7	~1	Н	н	-	7	(7	Н	7	7	7	N	N	~	7	г	N	N	~	7	7	7	7	7
		Match Length	Н	193	192	192	192	192	192	206	206	192	192	194	195	195	190	192	192	192	194	192	133	133	175	131	133	133	195	195	182	182	185
ð	Query	Match	94.8	94.8	85.8	85.2	81.1	79.2	œ.	•	77.7	77.7	77.3	76.9	76.3	76.3	76.1	76.1	76.1	76.1	76.1	75.6	73.8	73.3		69.8		ä	9	9	ف	26.5	è.
		Score	851	851	770.5	765.5	728	711	206	698	698	697.5		690.5	æ	685.5	683	683	683	683	683	619	663	658	638	627	607	554	241	241	238	238	238
	Result	No.	ч	7	æ	4	2	9	7	80			11	12	13	14	15	16	17	18	19	20	21	22	53	24	25	26	27	28	29	30	31

Aaq72467 fugu rubr Q9qv40 rattus sp.	Velyey gallus gall P42705 canis famil	P40225 homo sapien	Q8zdc8 yersinia pe	Aas62651 yersinia	Q8z2m5 salmonella	Q8zkz4 salmonella	Q7qdz2 anopheles q	Q87ay9 xylella fas	Q9hzm7 pseudomonas	Q8jeg9 human immun	P94873 lysobacter
AAQ72467 Q9QV40	TPO CANFA	TPO HUMAN	QBZDC8	AAS62651	Q8Z2M5	Q8ZKZ4	Q7QDZ2	Q87AY9	MURB PSEAE	Q8JE <u>G</u> 9	P94873
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185	352	353	323	323	346	346	432	154	339	861	3722
26.5	12:1	6.6	8.6	9.6	7.6	9.7	7.6	9.5	9.5	9.5	9.5
238 188	109	83	88	88	87.5	87.5	87.5	85.5	85	82	82
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## ALIGNMENTS

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EMBL, AF202301, AAF23132.1; JOINED.
EMBL, AF202310, AAF23133.1; -EMBL, AF202310, AAF23133.1; -EMBL, AF202311, AAF17572.1; -EMBL, AF202312, AAF23134.1; -EMBL, AF202312, AAF23134.1; JOINED.
EMBL, AF202312, AAF23134.1; JOINED.
EMBL, AF202312, AAF23134.1; JOINED.

S65458; AAD13964.1;

EMBL;

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Kobata A.;
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"Efficiency of signaling through cytokine receptors depends critically on receptor orientation.";

"Efficiency of signaling through cytokine receptors depends critically on receptor orientation.";

"INCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

"INCRELUIAR LOCATION: Secreted.

"INCRELUIAR LOCATION: Secreted.

"INCREME SPECIFICIAL: Broduced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.

"INCREME SPECIFICIAL: Used for the treatment of anemia. Available under the names Epogen (Amgen). Epogin (Chugai). Epomax (Elanex), Eprex (Janssen-Cilag), NeoRecormon or Recormon (Roche), and Procrit (Ortho Biotech). Variations in the glycosylation pattern of Epochic are generically known as epoetin alfa, NeoRecormon and Recormon as epoetin beta and Epomax as epoetin omega.

"INCREMENTALITY: Belongs to the EPO / TPO family.

"INCREMENTALITY: Belongs to the EPO / TPO family.

"INCREMENTALITY: NAME-Rel Systems. Com/asp/g_sitebuilder.asp?bodyId=197".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE OF CARBOHYDRATES.
MEDLINE=88153657; PubMed=3346214;
Takeuchi M., Takasaki S., Miyazaki H., Kato T., Hoshi S., Kochibe N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89118279; PubMed=3219367; Sasaki H., Ochi N., Dell A., Fukuda M.; Sate-specific glycosylation of human recombinant erythropoietin: analysis of glycopptides or peptides at each glycosylation site by East atom bombardment mass spectrometry."; Biochemistry 27:8618-8626(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative study of the asparagine-linked sugar chains of human erythropoietins purified from urine and the culture medium of excembinant Chinese hamster ovary cells.";
J. Biol. Chem. 263:367-3663(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=98445092; PubMed=9774108; DOI=10.1038/26773;
Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B.,
Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
Elliott S., Sirney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of human erythropoietin with monoclonal antibodies.";
J. Biol. Chem. 259:2707-2710(1984).
                                                                                                                                                                                                                                                                                                                 PRELIMINARY SEQUENCE OF 28-57.
MEDLINE=84135751; PubMed=6698989;
Yanagawa S., Hirade K., Ohnota H., Sasaki R., Chiba H., Ueda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structures and functional roles of the sugar chains of human
                                                                                                                       Lai P.H., Everett R., Wang F.F., Arakawa T., Goldwasser E., "Structural characterization of human erythropoietin."; J. Biol. Chem. 261:3116-3121(1986).
SEQUENCE OF 28-193, AND DISULFIDE BONDS
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MEDLINE=92314463; PubMed=1820196;
Takeuchi M., Kobata A.;
                                                                                 MEDLINE=86140080; PubMed=3949763;
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Glycobiology 1:337-346(1991)
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P -> Q (in an hepatocellular carcinoma).
/FTId=VAR_009871.
E -> Q (in Ref. 1; CAA26095).
Q -> QQ (in Ref. 5).
G -> R (in Ref. 1; CAA26095).
                                                                                                                                                                                                                                                                                                                Gaps
                                                     Removed in mature form (Probable).
                                                                                                                                                                   /FTId=CAR_000166.
N-linked (GlCNAc. ..).
/FTId=CAR_000192.
O-linked (GalNAc. ..).
SL -> NF (in an hepatocellular
                                                                                                                                                                                                                                                                                                      94.8%; Score 851; DB 1; Length 193; 100.0%; Pred. No. 2.3e-71;
                                                                                                                                                                                                                                                                                               21306 MW; C91F0E4C26A52033 CRC64;
                                                                                                                                                         /FTId=CAR 000052.
                                                                                                                                                       N-linked (GlcNAc.
                                                                                                                                      Erythropoietin.
                                                                                                                                                                                          carcinoma)
                                                                                                                                                                N-linked
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193 AA;
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Best Local &
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o. Indels 100.0%; Preca. ... 0; Mismatches Conservative Matches 166;

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EMBL; X02158; CAA26095.1; -.

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192 AA

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Erythropoietin precursor.
Name=EPO;
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les 154; Conservative
STANDARD;
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192
187
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192 AA;
                                                                                                                                                                                                            NCBI_TaxID=9541;
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CARBOHYD
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                                                                                                               88 VEVWQGLALISEAVLRGQALIVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEA1S 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                  28 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Doebber A., Elliott G., Jones T., Nguyen C., Stoneking T.,
"The sequence of Homo sapiens BAC clone RP11-336D7.";
".hitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPDAASAAPLRIITADTFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
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SEQUENCE 193 AA; 21307 MW; C91F0E4C26A52033 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 851; DB 2; __
Pred. No. 2.3e-71;
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100.0%; Pred. No.....
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson R.;
"Toward a complete human genome sequence.";
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                         193 AA
                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99063792; PubMed=9847074;
                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                     02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein EPO.
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Submitted (MAY-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens (Human)
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02-MAR-2004
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AC AAP2
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DT 02-PC
DE HYPC
OC BUKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=87055236; PubMed=2877922;

Lin F.-K., Lin C.-H., Lai P.-H., Browne J.K., Egrie J.C., Smalling R., Fox G.M., Chen K.K., Castro M., Suggs S.;

Monkey erythropoietin gene: cloning, expression and comparison with the human erythropoietin gene.";

Gene 44:201-209(1986).

-!- FUNCTION: Brythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of physiological level of circulating erythrocyte mass.

Physiological level of circulating erythrocyte mass.
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similarity).
similarity).
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-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PIR; JQ0173; JQ0173.
HSSP; P01588; 1CN4.
InterPro: IPR0090133; EPO TPO.
InterPro: IPR003013; ErVThroptn.
PEAM; PP60758; EPO TPO; 1.
PIRSF; PIRSF001931; EPO; 1.
PIRSF; PRRSF001931; EPO; 1.
PRINTS; PR00372; ERYTHROPTN.
PROSITE; PS00817; EPO_TPO; 1.
ETYTHROCYTE maturation; Glycoprotein; Hormone; Signal.
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Erythropoietin.
By similarity.
By similarity.
N-linked (GlCNAC. . . ) (EN Inhed (GLNAC. . . ) (EN Inhed (GalNAC. . . . ) (EN INHED (
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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A. M. Mucleotide sequence of equine erythropoietin and characterization of region-specific antibodies.";

I. Am. J. Vet. Res. 65:15-19(2004).

I. Am. J. Vet. Res. 65:15-19(2004).

R. M. J. Vet. Res. 65:15-19(2004).

R. HSSP, POLS88, 1BOY.

GO; GO:0005128; Ferythropoietin receptor binding; IEA.

GO; GO:0005129; Fibormon activity; IEA.

R. M. TherPro; IPR001013; EPO TPO.

R. InterPro; IPR001013; EPO TPO.

R. InterPro; IPR001013; EPO TPO.

R. InterPro; IPR001013; EPO TPO.

R. PIRSF PIRSF001551; EPO; I.

R. PRINF; PROF0151; EPO; I.

R. PRINF; PROF0175; ERYTHROPIN.

R. PROSITE; PS00817; EPO TPO; I.

R. SEQUENCE 192 AA; 20984 MW; E02D098490B09C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VEVWQGLALLISEAVLRGQALLIVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 APPRLICDSRVLERYILEAREAENVTMGCAEGCSFGENVTVPDTKVNFYSWRRMEVEQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                      142 Q-EAISLPDAASAAPLKTITADTFCKLFRVYSNFLRGKLKLYTGEACRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato F., Yamashita S., Kugo T., Hasegawa T., Mitsui I.,
Kijima-Suda I.;
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.9%; Pred. No. 7.3e-60;
Matches 141; Conservative 10; Mismatches 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 28, Created)
(Rel. 34, Last sequence update)
(Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                          Olovier,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (Rel. 44, Las
Erythropoietin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equue caballus (Horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
PubMed=14719696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erythropoietin.
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01-OCT-1996
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P33708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 PG----APPRLVCDSRVLERYLLEAKEAENVTMGCSESCSLNENITVPDTKVNFYAWKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence homology among mammals.";
Blood 82:1507-1516(1993).
-!- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
(By similarity).
(By similarity).
(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;
MEDLINE=33372347; PubMed=8364201;
MEDLINE=33372347; PubMed=8364201;
Wen D., Boiseel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czelusniak J., Goodman M., Burn H.F.;
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, L10609; AAA36842.1; -.
PIR; 164613; 184613.
HSSP; P01588; 1CM4.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001323; EPO TPO.
Pfam; P00758; EPO TPO; 1.
PRINTS; PRESF01951; ERYTHROPIN.
PRINTS; PR00135; ERYTHROPIN.
PROSITE; PS00131; EPO TPO; 1.
ERYTHROPIN.
PROSITE; PS00131; EPO TPO; 1.
ERYTHROCYTE maturation; Glycoprotein; Hormone; Signal.
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N-linked (GlCNAc...) (EN - 1 inked (GlCNAc...) (EN - 1 inked (GlCNAc...) (EN - 1 inked (GalNAc...) (EN - 1 inked (GalNAc...)) (EN - 1 inked (GalNAc...) (EN - 1 inked 
                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                      192 AA
                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
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                                                                                                                                                                                                                                                                                                               Erythropoietin precursor.
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9544;
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                                                                                                                                                                                                                                                                                                                                                 Name=EPO;
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                                                                                EPO_MACMU
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-192 FROM N.A.

MEDLINE-93372347; PubMed=8364201;

Men D., Boissel J.P.R. Tracy T.E., Mulcahy L.S., Czelusniak J.,

Goodman M., Bunn H.F.;

"Erythropoictin structure-function relationships: high degree of sequence homology among mammals.";

Blood 82:1507-1516(1993).

"FUNCTION: Erythropoictin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.

"FUNCELLULAR LOCATION: Secreted.

"SUBCELLULAR LOCATION: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals."

"In SISUE SPECIFICITY: Produced by Kidney or liver of adult mammals."

"In SIMILARITY: Belongs to the EPO / TPO family.
                                               Rattus, norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                 STRAIN=Wister; TISSUE=Kidney;
MEDLINE=93042015; PubMed=1420369;
Nagao M., Suga H., Okano M., Masuda S., Narita
                                                                                                                                                                                                                                                                               "Nucleotide sequence of rat erythropoietin.";
Biochim. Biophys. Acta 1171:99-102(1992).
         Erythropoietin precursor.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPRLICDSRVLERYLLEAKBAENITTGCAEHCSLNENITVPDTKVNFYAWKEMBVQQQA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 APPRLICDSRVLERYILGARBAENVTMGCAEGCSFSENITVPDTKVNFYTWKRMDVGQQA 86
                                                                                                                                                                                                                                                   -1- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of physiological level of circulating erythrocyte mass.
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted. Trissus Paper in the result of a secreted and by liver of fetal or neonatal mammals and by liver of fetal or neonatal mammals. SIMILARITY: Belongs to the EPO / TPO family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                     SEQUENCE OF 5-192 FROM N.A. MEDINE-93372347; PubMed-8364201; MEDLINE-93372347; PubMed-8364201; Men D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S., Czelusniak J., Goodman M., Bunn H.F., "Erythropoietin structure-function relationships: high degree of
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By similarity.
N-linked (GICNAC...) (Potential).
N-linked (GICNAC...) (Potential).
N-linked (GICNAC...) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
Goodman R.E., Bell R.G.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR
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PIRSF; PIRSF001951; EPO; 1.
PRINTS; PR00272; ERYTHROPTM.
PROSITE; PS00817; EPO TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone; Signal.
SIGNAL.
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Erythropoietin.
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PIR, 146083, 146083.
HSSP, P01588, 1BUY.
INTERPO: IPR003079; 4 helix cytokine.
InterPro; IPR001323; EPO TPO-
InterPro; IPR001323; EPO TPO-
InterPro; IPR001313; ENTERPOPEN.
                                                                                                                                                                                                   sequence homology among mammals.";
Blood 82:1507-1516(1993).
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33 187 BY
55 59 BY
64 64 NJ
109 109 NJ
144 44 G H
192 AA; 20914 MW; 6
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CARBOHYD
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CARBOHYD
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Best Local 8
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R HSSF; FULLOW,

R RGD; 2559; EBO.

DR InterPro; IPR001323; EPO_TPO.

DR InterPro; IPR001323; EPO_TPO.

DR InterPro; IPR001313; Erythroptn.

DR PEAM; PP00758; EPO_TPO; 1.

DR PROSITE; PR00272; ERYTHROPTN.

DR PROSITE; PR00817; EPO; 1.

DR PROSITE; PR00817; EPO; 1.

FT CIGNAL

FT CIRALN

FT CARBOHYD

FT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
EMBL; D10763; BAA01593.1; -. EMBL; L10608; AAA41126.1; -. PIR; S28148; S28148. HSSP; P01588; ICN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 82.5:
Les 137; Conservative
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EPO\_RAT STANDARD; PRT; 192 AA. P29676; P70504; 01-APR-1993 (Rel. 25, Created) 05-JUL-2004 (Rel. 44, Last annotation update)

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                                                                                  41 APPRLICDSRVIERYILEAREAENVTWGCAQGCSFSENITVPDTKVNFYTWKRMDVGQQA
                                                             VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96257233; PubMed=8666286; Suliman H.B., Majiwa P.A.O., Feldman B.F., Mertens B., Logan-Henfrey L.L.; Cloning of a cDMA encoding bovine erythropoietin and analysis of its transcription in selected tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 171:275-280(1996).

-!- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
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Exythropoietin.
By similarity.
By similarity.
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
N-linked (GloNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 697.5; DB 1; Length 192; Pred. No. 5.2e-57;
                                                                                                                                                                129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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EMBL; U44762; AAA86653.1; -.
HSSP; PO1588; 1CN4.
InterPro; IPR009099; 4 helix_cytokine.
InterPro; IPR001323; EPO TPO.
InterPro; IPR001313; Erythroptn.
Pfan; PP00758; EPO TPO; 1.
PIRSF; PIRSF01951; EPO; 1.
PRINTS; PROF01251; ERYTHROPTN.
PROSITE; PS00817; EPO_IPO; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Boran; TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                 Erythropoietin precursor.
Name=EPO;
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
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49
63
108
192 AA;
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                                                                                                                                                                                                                                                                                EPO BOVIN
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CARBOHYD
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                                                                                                                                                                                                                                         Canis familiaris (Dog).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erythropoietin.
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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0
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Souza D.S., Vicentim D.L., Costa F.F., Saad S.T.O.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; AY572971; AAS77874.1;
SEQUENCE 206 AA; 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 698; DB 2; Length 206; ilarity 81.3%; Pred. No. 5e-57; Conservative 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 PPDATQAAPLRILIADIFCKLFRVYSNFLRGKLKLYTGEACRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 PPDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
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                                                                                                                                                                                                                                                                                                                                                                               Souza D.S., Vicentim D.L., Costa P.F., Saad S.T.O.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS72971; ASS77874.1; -.
InterPro; IPR001959; 4 Helix_cytokine.
InterPro; IPR001233; EPO TPO.
InterPro; IPR0013031; Erythroptn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERMIT PRO0758; EPO TPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO TPO; 1.
SEQUENCE 206 AA; 22666 MW; IEEC64A02CE4F5B0 CRC64;
                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Erythropoietin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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15-APR-2004 (TrEMBLrel. 27,
15-APR-2004 (TrEMBLrel. 27,
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Best Local Similarity 81.3%
Matches 135; Conservative
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                                                                                                                         PRELIMINARY;
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wes 135; Conserv
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TISSUE=Kidney;
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15-APR-2004 (
15-APR-2004 (
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Q6PWUS;
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Matches
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                         192 AA;
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SEQUENCE FROM N.A.
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ID _ EPO_SHEEP
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Matches
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                                                                                         VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Abnormal erythropoietin (Epo) gene expression in the murine erythropoietin [Epo] results from a rearrangement between the G-
protein beta2 subunit gene and the Epo gene.";
Oncogene 15:1995-1999(1997).
-1- FUNCTION: Erythropoietin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-1- SUBCELLUIAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-1- SIMILARITY: Belongs to the EPO / TPO family.
                                       26 APARLICDSRVLERYILEAREAENATMGCAEGCSFNENITVPDTKVNFYAWKRMEVQQQA
                         9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.; "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7422 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker C.B., Mitsock L.D.; "Murine erythropoietin gene: cloning, expression, and human gene
  1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McDonald J.D., Lin F.-K., Goldwasser E., "Cloning, sequencing, and evolutionary analysis of the mouse exythropoietin gene.";
Mol. Cell. Biol. 6:842-848(1986).
                                                                                                                            129 PPDAA-SAAPLRIITADIFRKLFRVYSNFLRGKLKLYTGEACRIGDR 174
                                                                                                                                          146 LPDATPSAAPLRAFTVDALSKLFRIYSNFLRGKLTLYTGEACRRGDR 192
19; Indels
                                                                                                                                                                                                                                             01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
8; Mismatches
                                                                                                                                                                                                                       192
                                                                                                                                                                                                                    PRT;
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MEDLINE=21138439; PubMed=11239002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98030528; PubMed=9365246;
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87039105; PubMed=3773894;
                                                                                                                                                                                                                                                                                                                                                                                                                                homology.";
Mol. Cell. Biol. 6:849-858(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-52 FROM N.A.
                                                                                                                                                                                                                                                                                     Erythropoietin precursor.
Matches 139; Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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P07321:
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 APPRLICDSRVLERYILEAKEAENVTMGCAEGPRLSENITVPDTKVNFYAWKRMEVEEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 APPRLICDSRVLERYLLEAKEAENITIGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GlcNAc. . .) (By similarity). (GlcNAc. . .) (By similarity). (GlcNAc. . .) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93372547; PubMed≈8364201;
Wen D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 PPDTTPPAPLKTLTVDTFCKLFRVYANFLRGKLKLYTGEVCRRGDR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 694; DB 1; Lv 80.1%; Pred. No. 1.1e-56; Live 14; Mismatches 19;
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N-linked (GlCNAc..
N-linked (GlCNAc..
N-linked (GlCNAc..
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIRSF; PIRSF001951; BPO; 1.
PRINTS; PR00272; ERYTHROPTN.
PROSITE; PS00817; EPO TPO; 1.
Erythrocyte maturation; Glycoprotein; Hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P33709; 028572;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Wol. Cell. Endocrinol. 93:107-116(1993).
                                                                                                                                                                                                                                                             HSSP, P01588; 1CN4.

MGD; MGI:95407; Epo.

InterPro; 1PR009079; 4 helix_cytokine.

InterPro; 1PR001323; Epo_TPo.

InterPro; 1PR001313; Erythroptn.

Pfam; PF00758; Epo_TPo; 1.

PIRSF; PIRSF001951; EPO; 1.
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                                                                                                                          EMBL; M12482; AAA37568.1; -.
EMBL; M12930; AAA37570.1; -.
EMBL; AF312033; AAK28825.1; -.
EMBL; Y11971; CAA72707.1; -.
PIR; A24902; A24902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21365 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erythropoietin precursor.
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192
187
50
64
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69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 APARLICDSRVLERYILEAKEAENVTMGCAEGCSLGENITVPDTKVNFHHWKKSEAGRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.3%; Score 685.5; DB 2; Length 195; 81.4%; Pred. No. 7e-56; ive 12; Mismatches 18; Indels 1;
                                 MEDLINE=21200682; PubMed=11396976;

A Vilalta A., Wu D., Margalith M., Hobart P.;

Vilalta B., Wu D., Margalith M., Hobart P.;

E sochem. Biophys. Res. Commun. 284:823-827(2001).

R BEMBL: AR290441, AAG3662.1; -.

R BEMBL: AR290441, AAG3662.1; -.

R GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005128; F:erythropoietin receptor binding; IEA.

GO; GO:0005129; F:hormone activity; IEA.

R InterPro; IPR00309; 4 Helix cytokine.

R InterPro; IPR003013; EPO TPO; 1.

R PIRRE; PRRSF00135; EPO TPO; 1.
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R GG) GC10005576; Ccraracellular; IEA.

R GG) GC10005179; F:erythropoietin receptor binding; IEA.

R GO; GC10005179; F:hormone activity; IEA.

R GO; GC1005179; F:hormone activity; IEA.

BR InterPro; IRR003013; EPO_TPO.

BR InterPro; IRR003013; EPO_TPO.

BR PRESF: PIRSF: PR00372; ERVIHROPTN.

BR PRINTS; PR00372; ERVIHROPTN.

BR PROSITE; PS00817; EPO_TPO; 1.

BR PROSITE; PS00817; EPO_TPO; 1.
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Vilalta A., Wu D., Margalith M., Hobart P.;
"Rabbit EPO gene and cDNA: expression of rabbit EPO after
intramuscular injection of pDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0272; ERYTHROPIN.
PROSITE; PS00817; BPO TPO; 1.
SEQUENCE 195 AA; 21025 MW; 1FIDC7F403A303EC CRC64;
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EMBL; AF290943; AAG36961.1; -.
PIR; JC7699; JC7699.
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81.4%;
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Matches 136; Conservative
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                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erythropoietin.
Orytcolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria; Lagomorpha, Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROSCULIS, EXTROPTY.

PROSITE; PRO00372; EXTROPTY.

PROSITE; PRO00372; EXTROPTY.

PROSITE; PRO00372; EXTROPTY.

BY SIGNAL

CHAIN

28 194 BY Similarity.

CARBOHYD

CARBO
Czelusniak J., Goodman M., Bunn H.F.;
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 690.5; DB 1; Length 194; 82.0%; Pred. No. 2.4e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C025AAB0528131A9 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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9; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 146401; 146401.

HSSP; P01588; 1CM4.

InterPro; IPR009079; 4 helix_cytokine.

InterPro; IPR001323; EPO TPO.

InterPro; IPR001323; EYEhroptn.

Pfam; PF00758; EPO TPO; 1.

PIRSF; PIRSF001951; EPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z24681; CAA80848.1; -.
EMBL; L10610; AAA31518.1; -.
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Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                 99 VEVWQCLALLSEAMLRSQALLANSSQLPETLQVHVDKAVSGLRSLTSLLRALGVQKBAVS 148
                                                                                                                                                                69 VEVWOGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS 128
                                                     89
                                                                                   29 APARLICDSRVIERYILEAKEAENVTMGCAEGCSLGENITVPDTKVNFHHWKKSEAGRHA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence homology among mammals.";
Blood 82:1507-1516(1993).
-!- FUNCTION: Brythroopictin is the principal hormone involved in the regulation of erythrocyte differentiation and the maintenance of a physiological level of circulating erythrocyte mass.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Produced by kidney or liver of adult mammals and by liver of fetal or neonatal mammals.
-!- SIMILARITY: Belongs to the EPO / TPO family.
                                                  APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.

Erythropoietin.
By similarity.
By similarity.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Kidney;
MEDLINE=93372347; PubMed=8364201;
MEDLINE=93372347; PubMed=8364201;
MED D., Boissel J.P.R., Tracy T.E., Gruninger R.H., Mulcahy L.S.,
Czelusniak J., Goodman M., Bunn H.F.;
"Erythropoietin structure-function relationships: high degree of
                                                                                                                                                                                                                                                                                                               PPDAA-SAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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InterPro; IPR009079; 4 helix_cytokine.
InterPro; IPR01313; BPO_TPO.
InterPro; IPR003013; Brythroptn.
Pfam; PP00758; BPO_TPO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythropoietin precursor (Fragment)
  12;
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PROSITE; PS00817; EPO_TPO; 1
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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190
185
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        Matches 136;
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SIGNAL
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P49157;
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                                                                                                                                  69 VEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAIS
                                                                                   23 APPRLICDSRVLERYILEAKEGENATMGCAESCSFSENITVEDTKVNFYAWKRWEVQQQA
                                                              9 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYAWKRMEVGQQA
                                7
                                                                                                                                                                                                    129 PPDA--ASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR 174
                                                                                                                                                                                                                     143 LPDASPSSATPLRTFAVDTLCKLFRNYSNFLRGKLTLYTGEACRRRDR 190
 Length 190;
                                Indels
Score 683; DB 1;
Pred. No. 1.2e-55;
                                 7; Mismatches
   76.1%;
82.1%;
 Query Match
Best Local Similarity 82.1;
Matches 138; Conservative
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completed: November 19, 2004, 21:11:00 te : 104.996 secs